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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : <b>C07K 14/00</b>	A2	(11) International Publication Number: <b>WO 98/37094</b> (43) International Publication Date: 27 August 1998 (27.08.98)
(21) International Application Number: PCT/US98/03595 (22) International Filing Date: 24 February 1998 (24.02.98)  (30) Priority Data: 08/804,561 24 February 1997 (24.02.97) US 09/028,168 23 February 1998 (23.02.98) US  (71) Applicant: GENETICS INSTITUTE, INC. [US/US]; 87 CambridgePark Drive, Cambridge, MA 02140 (US).  (72) Inventors: JACOBS, Kenneth; 151 Beaumont Avenue, Newton, MA 02160 (US). MCCOY, John, M.; 56 Howard Street, Reading, MA 01867 (US). LAVALLIE, Edward, R.; 90 Green Meadow Drive, Tewksbury, MA 01876 (US). RACIE, Lisa, A.; 124 School Street, Acton, MA 01720 (US). MERBERG, David; 2 Orchard Drive, Acton, MA 01720 (US). TREACY, Maurice; 93 Walcott Road, Chestnut Hill, MA 02167 (US). SPAULDING, Vikki; 11 Meadowbank Road, Billerica, MA 01821 (US). AGOSTINO, Michael, J.; 26 Wolcott Avenue, Andover, MA 01810 (US).  (74) Agent: SPRUNGER, Suzanne, A.; Genetics Institute, Inc., 87 CambridgePark Drive, Cambridge, MA 02140 (US).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).  Published <i>Without international search report and to be republished upon receipt of that report.</i>
<p>(54) Title: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM</p> <p>(57) Abstract</p> <p>Novel polynucleotides and the proteins encoded thereby are disclosed.</p> <p>Plasmid name: pED8dpc2 Plasmid size: 5374 bp</p> <p>Comments/References: pED8dpc2 is derived from pED8dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kaufman et al.(1991), NAR 19: 4485-4490.</p>		

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## SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

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This application is a continuation-in-part of Ser. No. 60/XXX,XXX (converted to a provisional application from non-provisional application 08/804,561), filed February 24, 1997, which is incorporated by reference herein.

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FIELD OF THE INVENTION

The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

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BACKGROUND OF THE INVENTION

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 65 to nucleotide 1270;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 1139 to nucleotide 1270;
- 10 (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 1011 to nucleotide 1216;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BO114\_1 deposited under accession number ATCC 98333;
- 15 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BO114\_1 deposited under accession number ATCC 98333;
- (g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone BO114\_1 deposited under accession number ATCC 98333;
- 20 (h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone BO114\_1 deposited under accession number ATCC 98333;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
- 25 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 196 to amino acid 205 of SEQ ID NO:2;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- 30 (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and
- (m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 65 to nucleotide 1270; the nucleotide sequence of SEQ ID NO:1 from nucleotide 1139 to nucleotide 1270; the nucleotide sequence of SEQ ID NO:1 from nucleotide 1011 to nucleotide 1216; the nucleotide sequence of the full-length protein coding sequence of clone BO114\_1 deposited under accession number ATCC 98333; or the nucleotide sequence of the mature protein coding sequence of clone BO114\_1 deposited under accession number ATCC 98333. In other preferred embodiments, the polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of clone BO114\_1 deposited under accession number ATCC 98333. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2 from amino acid 326 to amino acid 384.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:2;
- (b) the amino acid sequence of SEQ ID NO:2 from amino acid 326 to amino acid 384;
- (c) fragments of the amino acid sequence of SEQ ID NO:2 comprising the amino acid sequence from amino acid 196 to amino acid 205 of SEQ ID NO:2; and
- (d) the amino acid sequence encoded by the cDNA insert of clone BO114\_1 deposited under accession number ATCC 98333;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2 or the amino acid sequence of SEQ ID NO:2 from amino acid 326 to amino acid 384.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 418 to nucleotide 582;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 508 to nucleotide 582;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 1 to nucleotide 555;

5 (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CD311\_2 deposited under accession number ATCC 98333;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CD311\_2 deposited under accession number ATCC 98333;

10 (g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone CD311\_2 deposited under accession number ATCC 98333;

(h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone CD311\_2 deposited under accession number ATCC 98333;

15 (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:4;

20 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and

25 (m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:3 from nucleotide 418 to nucleotide 582; the nucleotide sequence of SEQ ID NO:3 from nucleotide 508 to nucleotide 582; the nucleotide sequence of SEQ ID NO:3 from nucleotide 1 to nucleotide 555; the nucleotide sequence of the full-length protein coding sequence of clone CD311\_2 deposited under accession number ATCC 98333; or the nucleotide sequence of the mature protein coding sequence of clone CD311\_2 deposited under accession number ATCC 98333. In other preferred embodiments, the polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of

clone CD311\_2 deposited under accession number ATCC 98333. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4 from amino acid 1 to amino acid 46.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ 5 ID NO:3.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:4;
- 10 (b) the amino acid sequence of SEQ ID NO:4 from amino acid 1 to amino acid 46;
- (c) fragments of the amino acid sequence of SEQ ID NO:4 comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:4; and
- (d) the amino acid sequence encoded by the cDNA insert of clone 15 CD311\_2 deposited under accession number ATCC 98333;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4 or the amino acid sequence of SEQ ID NO:4 from amino acid 1 to amino acid 46.

In one embodiment, the present invention provides a composition comprising an 20 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 191 to nucleotide 1756;
- 25 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 254 to nucleotide 1756;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 1 to nucleotide 604;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CG279\_1 deposited under accession 30 number ATCC 98333;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CG279\_1 deposited under accession number ATCC 98333;

(g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone CG279\_1 deposited under accession number ATCC 98333;

5 (h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone CG279\_1 deposited under accession number ATCC 98333;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;

10 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 256 to amino acid 265 of SEQ ID NO:6;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

15 (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and

(m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5 from nucleotide 191 to nucleotide 1756; the nucleotide sequence of SEQ ID NO:5 from nucleotide 254 to nucleotide 1756; the nucleotide sequence of the full-length protein coding sequence of clone CG279\_1 deposited under accession number ATCC 98333; or the nucleotide sequence of the mature protein coding sequence of clone CG279\_1 deposited under accession number ATCC 98333. In other preferred embodiments, the 25 polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of clone CG279\_1 deposited under accession number ATCC 98333. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6 from amino acid 1 to amino acid 138.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ 30 ID NO:5.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:6;

(b) the amino acid sequence of SEQ ID NO:6 from amino acid 1 to amino acid 138;

(c) fragments of the amino acid sequence of SEQ ID NO:6 comprising the amino acid sequence from amino acid 256 to amino acid 265 of SEQ ID NO:6; and

(d) the amino acid sequence encoded by the cDNA insert of clone CG279\_1 deposited under accession number ATCC 98333; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:6 or the amino acid sequence of SEQ ID NO:6 from amino acid 1 to amino acid 138.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 226 to nucleotide 948;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 1128 to nucleotide 1601;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CJ424\_9 deposited under accession number ATCC 98333;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CJ424\_9 deposited under accession number ATCC 98333;

(f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone CJ424\_9 deposited under accession number ATCC 98333;

(g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone CJ424\_9 deposited under accession number ATCC 98333;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:8;

(j) a polynucleotide which is an allelic variant of a polynucleotide of  
5 (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein  
of (h) or (i) above ; and

5 (l) a polynucleotide capable of hybridizing under stringent conditions  
to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID  
NO:7 from nucleotide 226 to nucleotide 948; the nucleotide sequence of SEQ ID NO:7  
from nucleotide 1128 to nucleotide 1601; the nucleotide sequence of the full-length protein  
10 coding sequence of clone CJ424\_9 deposited under accession number ATCC 98333; or the  
nucleotide sequence of the mature protein coding sequence of clone CJ424\_9 deposited  
under accession number ATCC 98333. In other preferred embodiments, the  
polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of  
clone CJ424\_9 deposited under accession number ATCC 98333.

15 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
ID NO:7.

In other embodiments, the present invention provides a composition comprising  
a protein, wherein said protein comprises an amino acid sequence selected from the group  
consisting of:

20 (a) the amino acid sequence of SEQ ID NO:8;

(b) fragments of the amino acid sequence of SEQ ID NO:8 comprising  
the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:8;  
and

(c) the amino acid sequence encoded by the cDNA insert of clone

25 CJ424\_9 deposited under accession number ATCC 98333;

the protein being substantially free from other mammalian proteins. Preferably such  
protein comprises the amino acid sequence of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an  
isolated polynucleotide selected from the group consisting of:

30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:9;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:9 from nucleotide 137 to nucleotide 895;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 1488 to nucleotide 2274;

5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CR930\_1 deposited under accession number ATCC 98333;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CR930\_1 deposited under accession number ATCC 98333;

10 (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone CR930\_1 deposited under accession number ATCC 98333;

(g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone CR930\_1 deposited under accession number ATCC 98333;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

15 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 121 to amino acid 130 of SEQ ID NO:10;

(j) a polynucleotide which is an allelic variant of a polynucleotide of  
20 (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9 from nucleotide 137 to nucleotide 895; the nucleotide sequence of SEQ ID NO:9 from nucleotide 1488 to nucleotide 2274; the nucleotide sequence of the full-length protein coding sequence of clone CR930\_1 deposited under accession number ATCC 98333; or the nucleotide sequence of the mature protein coding sequence of clone CR930\_1 deposited  
30 under accession number ATCC 98333. In other preferred embodiments, the polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of clone CR930\_1 deposited under accession number ATCC 98333.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:9.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
- 5 (b) fragments of the amino acid sequence of SEQ ID NO:10 comprising the amino acid sequence from amino acid 121 to amino acid 130 of SEQ ID NO:10; and
- (c) the amino acid sequence encoded by the cDNA insert of clone CR930\_1 deposited under accession number ATCC 98333;
- 10 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:10.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 494 to nucleotide 973;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 611 to nucleotide 973;
- 20 (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 521 to nucleotide 940;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone DA306\_4 deposited under accession number ATCC 98333;
- 25 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone DA306\_4 deposited under accession number ATCC 98333;
- (g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone DA306\_4 deposited under accession number ATCC 98333;
- 30 (h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone DA306\_4 deposited under accession number ATCC 98333;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 75 to amino acid 84 of SEQ ID NO:12;

5 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and

10 (m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 494 to nucleotide 973; the nucleotide sequence of SEQ ID NO:11 from nucleotide 611 to nucleotide 973; the nucleotide sequence of SEQ ID NO:11 from nucleotide 521 to nucleotide 940; the nucleotide sequence of the full-length protein coding sequence of clone DA306\_4 deposited under accession number ATCC 98333; or the nucleotide sequence of the mature protein coding sequence of clone DA306\_4 deposited under accession number ATCC 98333. In other preferred embodiments, the polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of clone DA306\_4 deposited under accession number ATCC 98333. In yet other preferred 15 embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12 from amino acid 11 to amino acid 149.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:12;

(b) the amino acid sequence of SEQ ID NO:12 from amino acid 11 to 30 amino acid 149;

(c) fragments of the amino acid sequence of SEQ ID NO:12 comprising the amino acid sequence from amino acid 75 to amino acid 84 of SEQ ID NO:12; and

(d) the amino acid sequence encoded by the cDNA insert of clone DA306\_4 deposited under accession number ATCC 98333; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12 or the amino acid sequence 5 of SEQ ID NO:12 from amino acid 11 to amino acid 149.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 2295 to nucleotide 2594;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 1867 to nucleotide 2372;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone DG76\_1 deposited under accession number ATCC 98333;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone DG76\_1 deposited under accession number ATCC 98333;
- 20 (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone DG76\_1 deposited under accession number ATCC 98333;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone DG76\_1 deposited under accession number ATCC 98333;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:14;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(I) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:13 from nucleotide 2295 to nucleotide 2594; the nucleotide sequence of SEQ ID NO:13 from nucleotide 1867 to nucleotide 2372; the nucleotide sequence of the full-length protein coding sequence of clone DG76\_1 deposited under accession number ATCC 98333; or the nucleotide sequence of the mature protein coding sequence of clone DG76\_1 deposited under accession number ATCC 98333. In other preferred embodiments, the polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of clone DG76\_1 deposited under accession number ATCC 98333. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14 from amino acid 1 to amino acid 26.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:13.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
- (b) the amino acid sequence of SEQ ID NO:14 from amino acid 1 to amino acid 26;
- (c) fragments of the amino acid sequence of SEQ ID NO:14 comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:14; and
- (d) the amino acid sequence encoded by the cDNA insert of clone DG76\_1 deposited under accession number ATCC 98333;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:14 or the amino acid sequence of SEQ ID NO:14 from amino acid 1 to amino acid 26.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 394 to nucleotide 522;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 1 to nucleotide 476;

5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone DO19\_1 deposited under accession number ATCC 98333;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone DO19\_1 deposited under accession number ATCC 98333;

10 (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone DO19\_1 deposited under accession number ATCC 98333;

(g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone DO19\_1 deposited under accession number ATCC 98333;

15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 16 to amino acid 25 of SEQ ID NO:16;

20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

25 (l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 394 to nucleotide 522; the nucleotide sequence of SEQ ID NO:15 from nucleotide 1 to nucleotide 476; the nucleotide sequence of the full-length protein coding sequence of clone DO19\_1 deposited under accession number ATCC 98333; or the nucleotide sequence of the mature protein coding sequence of clone DO19\_1 deposited under accession number ATCC 98333. In other preferred embodiments, the polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of clone DO19\_1 deposited under accession number ATCC 98333. In yet other preferred

embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16 from amino acid 1 to amino acid 27.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ 5 ID NO:15.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
- 10 (b) the amino acid sequence of SEQ ID NO:16 from amino acid 1 to amino acid 27;
- (c) fragments of the amino acid sequence of SEQ ID NO:16 comprising the amino acid sequence from amino acid 16 to amino acid 25 of SEQ ID NO:16; and
- 15 (d) the amino acid sequence encoded by the cDNA insert of clone DO19\_1 deposited under accession number ATCC 98333;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16 or the amino acid sequence of SEQ ID NO:16 from amino acid 1 to amino acid 27.

20 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID 25 NO:17 from nucleotide 262 to nucleotide 654;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 322 to nucleotide 654;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 1 to nucleotide 618;
- 30 (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone EQ219\_1 deposited under accession number ATCC 98333;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone EQ219\_1 deposited under accession number ATCC 98333;

(g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone EQ219\_1 deposited under accession number ATCC 98333;

5 (h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone EQ219\_1 deposited under accession number ATCC 98333;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;

10 (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 60 to amino acid 69 of SEQ ID NO:18;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

15 (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and

(m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:17 from nucleotide 262 to nucleotide 654; the nucleotide sequence of SEQ ID NO:17 from nucleotide 322 to nucleotide 654; the nucleotide sequence of SEQ ID NO:17 from nucleotide 1 to nucleotide 618; the nucleotide sequence of the full-length protein coding sequence of clone EQ219\_1 deposited under accession number ATCC 98333; or the nucleotide sequence of the mature protein coding sequence of clone EQ219\_1 deposited under accession number ATCC 98333. In other preferred embodiments, the 20 polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of clone EQ219\_1 deposited under accession number ATCC 98333. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18 from amino acid 1 to amino acid 119.

25 30 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:17.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:18;

(b) the amino acid sequence of SEQ ID NO:18 from amino acid 1 to amino acid 119;

5 (c) fragments of the amino acid sequence of SEQ ID NO:18 comprising the amino acid sequence from amino acid 60 to amino acid 69 of SEQ ID NO:18; and

(d) the amino acid sequence encoded by the cDNA insert of clone EQ219\_1 deposited under accession number ATCC 98333;

the protein being substantially free from other mammalian proteins. Preferably such 10 protein comprises the amino acid sequence of SEQ ID NO:18 or the amino acid sequence of SEQ ID NO:18 from amino acid 1 to amino acid 119.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 74 to nucleotide 310;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 125 to nucleotide 310;

20 (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 1 to nucleotide 338;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone FG340\_1 deposited under accession number ATCC 98333;

25 (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone FG340\_1 deposited under accession number ATCC 98333;

(g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone FG340\_1 deposited under accession number ATCC 98333;

30 (h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone FG340\_1 deposited under accession number ATCC 98333;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:20;

5 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and

(m) a polynucleotide capable of hybridizing under stringent conditions  
10 to any one of the polynucleotides specified in (a)-(j).

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:19 from nucleotide 74 to nucleotide 310; the nucleotide sequence of SEQ ID NO:19 from nucleotide 125 to nucleotide 310; the nucleotide sequence of SEQ ID NO:19 from nucleotide 1 to nucleotide 338; the nucleotide sequence of the full-length protein coding sequence of clone FG340\_1 deposited under accession number ATCC 98333; or the nucleotide sequence of the mature protein coding sequence of clone FG340\_1 deposited under accession number ATCC 98333. In other preferred embodiments, the polynucleotide encodes the full-length or mature protein encoded by the cDNA insert of clone FG340\_1 deposited under accession number ATCC 98333. In yet other preferred  
15 embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20 from amino acid 1 to amino acid 75.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:19.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:20;

(b) the amino acid sequence of SEQ ID NO:20 from amino acid 1 to  
30 amino acid 75;

(c) fragments of the amino acid sequence of SEQ ID NO:20 comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:20;  
and

(d) the amino acid sequence encoded by the cDNA insert of clone FG340\_1 deposited under accession number ATCC 98333; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:20 or the amino acid sequence 5 of SEQ ID NO:20 from amino acid 1 to amino acid 75.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial, yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the present invention are organisms that have enhanced, reduced, or 10 modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

- (a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and
- 15 (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention. Preferred embodiments include those in which the protein produced by such process is a mature form of the protein.

Protein compositions of the present invention may further comprise a 20 pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a 25 pharmaceutically acceptable carrier.

#### BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

30

#### DETAILED DESCRIPTION

##### ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide

sequence of each clone can readily be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full-length and mature) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by  
5 expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing.

As used herein a "secreted" protein is one which, when expressed in a suitable host  
10 cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

15

Clone "BO114\_1"

A polynucleotide of the present invention has been identified as clone "BO114\_1". BO114\_1 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
20 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BO114\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BO114\_1 protein").

The nucleotide sequence of BO114\_1 as presently determined is reported in SEQ  
25 ID NO:1. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BO114\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2. Amino acids 346 to 358 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 359, or are a transmembrane domain.

30 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BO114\_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for BO114\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BO114\_1 demonstrated at least some similarity with sequences

identified as AA430329 (zw20e04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 769854 5' similar to contains element MER22 repetitive element), H00825 (yj31b05.r1 Homo sapiens cDNA clone 150321 5'), H12557 (yj12c09.r1 Homo sapiens cDNA clone 148528 5'), W53899 (md09c01.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA), and Z82202 (Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 34P24). Based upon sequence similarity, BO114\_1 proteins and each similar protein or peptide may share at least some activity.

Clone "CD311\_2"

10 A polynucleotide of the present invention has been identified as clone "CD311\_2". CD311\_2 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CD311\_2 is a full-length 15 clone, including the entire coding sequence of a secreted protein (also referred to herein as "CD311\_2 protein").

The nucleotide sequence of CD311\_2 as presently determined is reported in SEQ ID NO:3. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CD311\_2 protein corresponding to the foregoing 20 nucleotide sequence is reported in SEQ ID NO:4. Amino acids 18 to 30 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 31, or are a transmembrane domain.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CD311\_2 should be approximately 2400 bp.

25 The nucleotide sequence disclosed herein for CD311\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CD311\_2 demonstrated at least some similarity with sequences identified as H17421 (ym40d12.s1 Homo sapiens cDNA clone 50810 3'), H20618 (ym47b01.r1 Homo sapiens cDNA clone 51411 5'), and U70476 (Rattus norvegicus cationic 30 amino acid transporter-1 (CAT-1) mRNA, complete cds). Based upon sequence similarity, CD311\_2 proteins and each similar protein or peptide may share at least some activity.

Clone "CG279\_1"

A polynucleotide of the present invention has been identified as clone "CG279\_1". CG279\_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was 5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CG279\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CG279\_1 protein").

The nucleotide sequence of CG279\_1 as presently determined is reported in SEQ 10 ID NO:5. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CG279\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6. Amino acids 9 to 21 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22, or are a transmembrane domain. Amino acids 43 to 55 are a possible 15 leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 56, or are a transmembrane domain

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CG279\_1 should be approximately 3940 bp.

The nucleotide sequence disclosed herein for CG279\_1 was searched against the 20 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CG279\_1 demonstrated at least some similarity with sequences identified as AA568111 (nf13c05.s1 NCI\_CGAP\_Pr1 Homo sapiens cDNA clone IMAGE:913640), D63222 (Human placenta cDNA 5'-end GEN-508F12), H64777 (yu62h09.r1 Homo sapiens cDNA clone 238433 5' similar to contains Alu repetitive 25 element;contains TAR1 repetitive element), M17262 (Human prothrombin (F2) gene, complete cds, and Alu and KpnI repeats), Q39724 (Expressed Sequence Tag human gene marker EST00316), U14685 (Gorilla gorilla Alu-Sb2 repeat, clone GO-14), U14691 (Gorilla gorilla Alu-Sb2 repeat, clone GOI2-11), and W15458 (zc19h02.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 322803 3'). The predicted amino acid sequence 30 disclosed herein for CG279\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CG279\_1 protein demonstrated at least some similarity to sequences identified as D25215 (KIAA0032 [Homo sapiens]), M15530 (B-cell growth factor [Homo sapiens]), and R95913 (Neural thread protein). Based upon sequence similarity, CG279\_1 proteins and each similar

protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the CG279\_1 protein sequence, centered around amino acids 30, 250, and 390 of SEQ ID NO:6, respectively. The nucleotide sequence of CG279\_1 indicates that it may contain one or more Alu repetitive elements.

Clone "CJ424\_9"

A polynucleotide of the present invention has been identified as clone "CJ424\_9". CJ424\_9 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CJ424\_9 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CJ424\_9 protein").

The nucleotide sequence of CJ424\_9 as presently determined is reported in SEQ ID NO:7. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CJ424\_9 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:8.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CJ424\_9 should be approximately 1650 bp.

The nucleotide sequence disclosed herein for CJ424\_9 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CJ424\_9 demonstrated at least some similarity with sequences identified as AB000215 (*Rattus norvegicus* cca1 mRNA, complete cds) and R83763 (yp16f06.s1 *Homo sapiens* cDNA clone 187619 3'). The predicted amino acid sequence disclosed herein for CJ424\_9 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CJ424\_9 protein demonstrated at least some similarity to sequences identified as AB000215 (CCA1 protein [*Rattus norvegicus*]) and M59465 (A20 [*Homo sapiens*] ). Based upon sequence similarity, CJ424\_9 proteins and each similar protein or peptide may share at least some activity.

Clone "CR930\_1"

A polynucleotide of the present invention has been identified as clone "CR930\_1". CR930\_1 was isolated from a human adult testes cDNA library using methods which are

selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CR930\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein 5 as "CR930\_1 protein").

The nucleotide sequence of CR930\_1 as presently determined is reported in SEQ ID NO:9. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CR930\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10.

10 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CR930\_1 should be approximately 2400 bp.

The nucleotide sequence disclosed herein for CR930\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CR930\_1 demonstrated at least some similarity with sequences 15 identified as AA058338 (zk82e08.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 489350 3'), N54229 yz03f05.r1 Homo sapiens cDNA clone), R89733 (ym99e10.r1 Homo sapiens cDNA clone 167082 5'), and W60141 (zc94f06.s1 Pancreatic Islet Homo sapiens cDNA clone 338819 3'). The predicted amino acid sequence disclosed herein for CR930\_1 was searched against the GenPept and GeneSeq amino acid sequence databases 20 using the BLASTX search protocol. The predicted CR930\_1 protein demonstrated at least some similarity to sequences identified as a *C. elegans* ORF (open reading frame) (U21324) that is weakly similar to *S. cerevisiae* CBP3 protein precursor (SP:CBP3\_YEAST, P21560), a mitochondrial membrane protein. Based upon sequence similarity, CR930\_1 proteins and each similar protein or peptide may share at least some activity.

25

Clone "DA306\_4"

A polynucleotide of the present invention has been identified as clone "DA306\_4". DA306\_4 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was 30 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. DA306\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "DA306\_4 protein").

The nucleotide sequence of DA306\_4 as presently determined is reported in SEQ ID NO:11. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the DA306\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:12. Amino acids 27 to 39 are a predicted 5 leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 40; or are a transmembrane domain.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone DA306\_4 should be approximately 2800 bp.

The nucleotide sequence disclosed herein for DA306\_4 was searched against the 10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. DA306\_4 demonstrated at least some similarity with sequences identified as AA397398 (nc65a07.r1 NCI CGAP Pr1 Homo sapiens cDNA clone 771444), AL008629 (Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 197O17; HTGS phase 1), D78769 (Human placenta cDNA 5'-end GEN-512A03), M19364 15 (Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds), N29380 (yw97f09.s1 Homo sapiens cDNA clone 260201 3'), N47928 (yw97f09.r1 Homo sapiens cDNA clone 260201 5'), Z83745 (Human DNA sequence from PAC 453A3 contains EST and STS), and Z83848 (Human DNA sequence \*\*\* SEQUENCING IN PROGRESS \*\*\* from clone 57A13; HTGS phase 1). The predicted 20 amino acid sequence disclosed herein for DA306\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted DA306\_4 protein demonstrated at least some similarity to sequences identified as M12140 (envelope protein [Homo sapiens]), M19051 (pol protein [Mus musculus]), R75189 (Osteoinductive retrovirus RFB-14 pol gene product), U88902 (integrase [Homo 25 sapiens]). Based upon sequence similarity, DA306\_4 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of DA306\_4 indicates that it may contain a CpG island repeat region.

Clone "DG76\_1"

30 A polynucleotide of the present invention has been identified as clone "DG76\_1". DG76\_1 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. DG76\_1 is a full-length clone,

including the entire coding sequence of a secreted protein (also referred to herein as "DG76\_1 protein").

The nucleotide sequence of DG76\_1 as presently determined is reported in SEQ ID NO:13. What applicants presently believe to be the proper reading frame and the 5 predicted amino acid sequence of the DG76\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone DG76\_1 should be approximately 3300 bp.

The nucleotide sequence disclosed herein for DG76\_1 was searched against the 10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. DG76\_1 demonstrated at least some similarity with sequences identified as AA044352 (zk54c01.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486624 5') and N57171 (yw90f09.r1 Homo sapiens cDNA clone 259529 5'). Based upon sequence similarity, DG76\_1 proteins and each similar protein or peptide may share 15 at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the DG76\_1 protein sequence, centered amino acids 15 and 80 of SEQ ID NO:14, respectively. The nucleotide sequence of DG76\_1 indicates that it may contain a MER repeat region.

20           Clone "DO19\_1"

A polynucleotide of the present invention has been identified as clone "DO19\_1". DO19\_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer 25 analysis of the amino acid sequence of the encoded protein. DO19\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "DO19\_1 protein").

The nucleotide sequence of DO19\_1 as presently determined is reported in SEQ ID NO:15. What applicants presently believe to be the proper reading frame and the 30 predicted amino acid sequence of the DO19\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone DO19\_1 should be approximately 700 bp.

The nucleotide sequence disclosed herein for DO19\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. DO19\_1 demonstrated at least some similarity with sequences identified as AA339440 (EST44546 Fetal brain I Homo sapiens cDNA 5' end). Based upon 5 sequence similarity, DO19\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of DO19\_1 indicates that it may contain one or more MER20 repetitive elements.

Clone "EQ219\_1"

10 A polynucleotide of the present invention has been identified as clone "EQ219\_1". EQ219\_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. EQ219\_1 is a full-length 15 clone, including the entire coding sequence of a secreted protein (also referred to herein as "EQ219\_1 protein").

The nucleotide sequence of EQ219\_1 as presently determined is reported in SEQ ID NO:17. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the EQ219\_1 protein corresponding to the foregoing 20 nucleotide sequence is reported in SEQ ID NO:18. Amino acids 8 to 20 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21, or are a transmembrane domain.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone EQ219\_1 should be approximately 800 bp.

25 The nucleotide sequence disclosed herein for EQ219\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. EQ219\_1 demonstrated at least some similarity with sequences identified as AA400429 (zu62a09.s1 Soares testis NHT Homo sapiens cDNA clone 742552 3'). Based upon sequence similarity, EQ219\_1 proteins and each similar protein or peptide 30 may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the EQ219\_1 protein sequence, centered around amino acid 90 of SEQ ID NO:18.

Clone "FG340\_1"

A polynucleotide of the present invention has been identified as clone "FG340\_1". FG340\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was 5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. FG340\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "FG340\_1 protein").

The nucleotide sequence of FG340\_1 as presently determined is reported in SEQ 10 ID NO:19. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the FG340\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:20. Amino acids 5 to 17 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18, or are a transmembrane domain.

15 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone FG340\_1 should be approximately 900 bp.

The nucleotide sequence disclosed herein for FG340\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. FG340\_1 demonstrated at least some similarity with sequences 20 identified as N59424 (yv51g05.s1 Homo sapiens cDNA clone 246296 3'). The FG340\_1 nucleotide sequence has an interesting simple "TG" nucleotide repeat from basepair 96 to basepair 131 of SEQ ID NO:19. This region encodes a Cys-Val repeat in the FG340\_1 protein. Similar Cys-Val stretches are found in the amino termini of X52164 (Q300 protein (AA 1-77) [Mus musculus]) and M37679 (Ig heavy chain precursor [Mus musculus]). 25 Based upon sequence similarity, FG340\_1 proteins and each similar protein or peptide may share at least some activity.

Deposit of Clones

Clones BO114\_1, CD311\_2, CG279\_1, CJ424\_9, CR930\_1, DA306\_4, DG76\_1, 30 DO19\_1, EQ219\_1, and FG340\_1 were deposited on February 20, 1997 with the American Type Culture Collection as an original deposit under the Budapest Treaty and were given the accession number ATCC 98333, from which each clone comprising a particular polynucleotide is obtainable. All restrictions on the availability to the public of the

deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b).

Each clone has been transfected into separate bacterial cells (*E. coli*) in this composite deposit. Each clone can be removed from the vector in which it was deposited

5 by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Fig. 1. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* 19: 4485-4490); the pNOTs vector was derived from pMT2

10 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* 9: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site

15 and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite

20 deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of the oligonucleotide probe that was used to isolate each full-length clone is identified below,

25 and should be most reliable in isolating the clone of interest.

<u>Clone</u>	<u>Probe Sequence</u>
BO114_1	SEQ ID NO:21
CD311_2	SEQ ID NO:22
30 CG279_1	SEQ ID NO:23
CJ424_9	SEQ ID NO:24
CR930_1	SEQ ID NO:25
DA306_4	SEQ ID NO:26
DG76_1	SEQ ID NO:27

DO19_1	SEQ ID NO:28
EQ219_1	SEQ ID NO:29
FG340_1	SEQ ID NO:30

5 In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoamidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

10 The design of the oligonucleotide probe should preferably follow these parameters:

- (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;
- (b) It should be designed to have a  $T_m$  of approx. 80 ° C (assuming 2° for each

15 A or T and 4 degrees for each G or C).

The oligonucleotide should preferably be labeled with  $\text{g}^{-32}\text{P}$  ATP (specific activity 6000 Ci/mmole) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4e+6 dpm/pmole.

20 The bacterial culture containing the pool of full-length clones should preferably be thawed and 100  $\mu\text{l}$  of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100  $\mu\text{g}/\text{ml}$ . The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100  $\mu\text{g}/\text{ml}$  and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

25 30 Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 µg/ml of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at 5 a concentration greater than or equal to 1e+6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The 10 filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, 15 hybridization analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. 20 McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion 25 could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence 30 listing by translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* 15(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* 62(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, *Bioessays* 14(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* 90(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination,

preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably 5 are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), 10 the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

15 Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing 20 the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most 25 preferably at least 95% identity) with any such segment of any of the disclosed proteins.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or 30 polynucleotide, as determined by those of skill in the art. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologs are those isolated from mammalian species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous, or related to that encoded by the polynucleotides .

5        The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency  
10      conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) <sup>t</sup>	Hybridization Temperature and Buffer <sup>t</sup>	Wash Temperature and Buffer <sup>t</sup>
5	A	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	<50	T <sub>B</sub> *; 1xSSC	T <sub>B</sub> *; 1xSSC
	C	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	<50	T <sub>D</sub> *; 1xSSC	T <sub>D</sub> *; 1xSSC
	E	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	<50	T <sub>F</sub> *; 1xSSC	T <sub>F</sub> *; 1xSSC
10	G	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	<50	T <sub>H</sub> *; 4xSSC	T <sub>H</sub> *; 4xSSC
	I	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	<50	T <sub>J</sub> *; 4xSSC	T <sub>J</sub> *; 4xSSC
	K	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	<50	T <sub>L</sub> *; 2xSSC	T <sub>L</sub> *; 2xSSC
15	M	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	<50	T <sub>N</sub> *; 6xSSC	T <sub>N</sub> *; 6xSSC
	O	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
	P	<50	T <sub>P</sub> *; 6xSSC	T <sub>P</sub> *; 6xSSC
	Q	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	<50	T <sub>R</sub> *; 4xSSC	T <sub>R</sub> *; 4xSSC

<sup>t</sup>: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

<sup>t</sup>: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH<sub>2</sub>PO<sub>4</sub>, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

30 \*T<sub>B</sub> - T<sub>R</sub>: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T<sub>m</sub>) of the hybrid, where T<sub>m</sub> is determined according to the following equations. For hybrids less than 18 base pairs in length, T<sub>m</sub>(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T<sub>m</sub>(°C) = 81.5 + 16.6(log<sub>10</sub>[Na<sup>+</sup>]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na<sup>+</sup>] is the concentration of sodium ions in the hybridization buffer ([Na<sup>+</sup>] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds.,

5 John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 10 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide of the invention may be operably linked to an 15 expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman et al., Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably 20 linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the 25 protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

30 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial

strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or  
5 enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from,  
10 e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."  
15 The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column  
20 containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.  
25 Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and  
30 InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant

methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance  
5 with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

10 The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith,  
15 including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally  
20 provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another  
25 amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be  
30 expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

**USES AND BIOLOGICAL ACTIVITY**

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

**Research Uses and Utilities**

10        The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

15        20        25        30        The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which

the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the

5 protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent  
10 grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to  
15 Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

#### Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein  
20 or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention  
25 can be added to the medium in or on which the microorganism is cultured.

#### Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may  
30 induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays

for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured  
5 by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 10 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node 15 cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon  $\gamma$ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic 20 cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 25 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human 30 Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies,  
5 E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immunol. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol.  
10 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays  
15 are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal  
20 infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also  
25 be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation,  
30 Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for

example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an

5 immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves

10 inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

15 Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue

20 transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a

25 monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an

30 immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or

tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in

5 humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed.,

10 Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate

15 activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell

20 activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of

25 human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

30 Uregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Uregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of

viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient

- 5 by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfet them with a nucleic
- 10 acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function

- 15 (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides.
- 20 For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used
- 25 to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II

- 30 molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$  microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface.

Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such 5 as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

10 The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates 15 and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 20 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching 25 (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

30 Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter

7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

#### Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent

myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of 5 hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or 10 *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

15 Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et 20 al., *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of 25 Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 30 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland,

H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

5 A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth  
10 in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of  
15 congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce  
20 differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

25 Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and  
30 other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of

congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting

5 differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described

10 in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium ).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year  
15 Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

#### Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- $\beta$  group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example,

20 United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

30

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

5

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells.

10 Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses

15 against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population

20 of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent

25 chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene

30 Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thromolytic Activity

A protein of the invention may also exhibit hemostatic or thromolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation 5 and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

10 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thromolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 15 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of 20 such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and 25 development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

30 The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and

Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 5 1995.

#### Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in 10 the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat 15 inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting 20 from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

#### Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major 25 roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

30 The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the

first cadherin domain provide the basis for homophilic adhesion; modification of this recognition site can change the specificity of a cadherin so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

5 E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to  
10 their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention  
15 encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue  
20 in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and  
25 polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the  
30 cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used

to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides 5 encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

10           Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or 15 tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

20           Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, 25 weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, 30 carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic

lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen

5   in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

#### ADMINISTRATION AND DOSING

10   A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term

15   "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11,

20   IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention,

25   or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

30   A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T 5 lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that 10 can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome 15 in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, 20 and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total 25 amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to 30 a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be

administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be  
5 administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic  
10 factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection.

15 Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or  
20 an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain  
25 physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

30 When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred

pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The

5 pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone.

10 Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1ng to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein of the present invention per kg body weight.

15 The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

20 Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal

antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting 5 and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When 10 administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also 15 optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the 20 developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular 25 application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins 30 or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-

aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns.

5 In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, 10 ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropylmethylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 15 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

20 In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

25 The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering 30 various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in

the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

15 Patent and literature references cited herein are incorporated by reference as if fully set forth.

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Jacobs, Kenneth  
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(ii) TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
ENCODING THEM

(iii) NUMBER OF SEQUENCES: 30

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Sprunger, Suzanne A.  
(B) REGISTRATION NUMBER: 41,323

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## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1551 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTGTTATTGT AGCGAGGGAC ATGAGCTGGA GGCTGATGGC ATCAGCTGCA GCCCTGCAGG	60
GGCCATGGGT GCCCAGGCTT CCCAGGACCT CGGAGATGAG TTGCTGGATG ACGGGGAGGA	120
TGAGGAAGAT GAAGACGAGG CCTGGAAGGC CTTCAACGGT GGCTGGACGG AGATGCCTGG	180
GATCCTGTGG ATGGAGCCTA CGCAGCCGCC TGACTTTGCC CTGGCCTATA GACCGAGCTT	240
CCCAGAGGAC AGAGAGCCAC AGATAACCTA CCCGGAGCCC ACCTGGCCAC CCCCAGCTCAG	300
TGCCCCCAGG GTCCCCCTACC ACTCCTCAGT GCTCTCCGTC ACCCGGCCTG TGGTGGTCTC	360
TGCCACGCGT CCCACACTGC CTTCTGCCA CCAGCCTCCT GTGATCCCTG CCACACACCC	420
AGCTTTGTCC CGTGACCACC AGATCCCCGT GATCGCAGCC AACTATCCAG ATCTGCCTTC	480
TGCCTACCAA CCCGGTATTC TCTCTGTCTC TCATTAGCA CAGCCTCCTG CCCACCAGCC	540
CCCTATGATC TCAACCAAAT ATCCGGAGCT CTTCCCTGCC CACCAGTCCC CCATGTTCC	600
AGACACCCGG GTCGCTGGCA CCCAGACCAC CACTCATTTG CCTGGAATCC CACCTAACCA	660
TGCCCCCTTG GTCACCACCC TCGGTGCCA GCTACCCCT CAAGCCCCAG ATGCCCTTG	720
CCTCAGAACCC CAGGCCACCC AGCTCCCAT TATCCCAACT GCCCAGCCCT CTCTGACCAC	780
CACCTCCAGG TCCCCCTGTG CTCCTGCCA TCAAATCTCT GTGCCTGCTG CCACCCAGCC	840
CGCAGCCCTC CCCACCCCTC TGCCCTCTCA GAGCCCCACT AACCAAGACCT CACCCATCAG	900
CCCTACACAT CCCCCATTCCA AAGCCCCCA AATCCCAAGG GAAGATGGCC CCAGTCCCAA	960
GTTGGCCCTG TGGCTGCCCT CACCAGCTCC CACAGCAGCC CCAACAGCCC TGGGGGAGGC	1020
TGGTCTTGCC GAGCACAGCC AGAGGGATGA CCGGTGGCTG CTGGTGGCAC TCCCTGGTGCC	1080
AACGTGTGTC TTTTTGGTGG TCCTGCTTG ACTGGGCATC GTGTACTGCA CCCGCTGTGG	1140
CCCCCATGCA CCCAACAAAGC GCATCACTGA CTGCTATCGC TGGGTCACTCC ATGCTGGGAG	1200
CAAGAGCCCA ACAGAACCCA TGCCCCCCAG GGGCAGCCTC ACAGGGGTGC AGACCTGCAG	1260
AACCAGCGTG TGATGGGGTG CAGACCCCCC TCATGGAGTA TGGGGCGCTG GACACATGGC	1320
CGGGGCTGCA CCAGGGACCC ATGGGGGCTG CCCAGCTGGA CAGATGGCTT CCTGCTCCCC	1380
AGGGCCAGCC AGGGTCCCTCT CTCAACCACT AGACTTGGCT CTCAGGAACCT CTGCTTCCCTG	1440

GCCCAGCGCT CGTGACCAAG GATACACCAA AGCCCTTAAG ACCTCAGGGG GCGGGTGCTG	1500
GGGTCTTCTC CAATAAATGG GGTGTCAACC TTAAAAAAAAA AAAAAAAAAA A	1551

## (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ala Gln Ala Ser Gln Asp Leu Gly Asp Glu Leu Leu Asp Asp			
1	5	10	15
Gly Glu Asp Glu Glu Asp Glu Asp Glu Ala Trp Lys Ala Phe Asn Gly			
20	25	30	
Gly Trp Thr Glu Met Pro Gly Ile Leu Trp Met Glu Pro Thr Gln Pro			
35	40	45	
Pro Asp Phe Ala Leu Ala Tyr Arg Pro Ser Phe Pro Glu Asp Arg Glu			
50	55	60	
Pro Gln Ile Pro Tyr Pro Glu Pro Thr Trp Pro Pro Pro Leu Ser Ala			
65	70	75	80
Pro Arg Val Pro Tyr His Ser Ser Val Leu Ser Val Thr Arg Pro Val			
85	90	95	
Val Val Ser Ala Thr Arg Pro Thr Leu Pro Ser Ala His Gln Pro Pro			
100	105	110	
Val Ile Pro Ala Thr His Pro Ala Leu Ser Arg Asp His Gln Ile Pro			
115	120	125	
Val Ile Ala Ala Asn Tyr Pro Asp Leu Pro Ser Ala Tyr Gln Pro Gly			
130	135	140	
Ile Leu Ser Val Ser His Ser Ala Gln Pro Pro Ala His Gln Pro Pro			
145	150	155	160
Met Ile Ser Thr Lys Tyr Pro Glu Leu Phe Pro Ala His Gln Ser Pro			
165	170	175	
Met Phe Pro Asp Thr Arg Val Ala Gly Thr Gln Thr Thr His Leu			
180	185	190	

Pro Gly Ile Pro Pro Asn His Ala Pro Leu Val Thr Thr Leu Gly Ala  
 195 200 205  
 Gln Leu Pro Pro Gln Ala Pro Asp Ala Leu Val Leu Arg Thr Gln Ala  
 210 215 220  
 Thr Gln Leu Pro Ile Ile Pro Thr Ala Gln Pro Ser Leu Thr Thr Thr  
 225 230 235 240  
 Ser Arg Ser Pro Val Ser Pro Ala His Gln Ile Ser Val Pro Ala Ala  
 245 250 255  
 Thr Gln Pro Ala Ala Leu Pro Thr Leu Leu Pro Ser Gln Ser Pro Thr  
 260 265 270  
 Asn Gln Thr Ser Pro Ile Ser Pro Thr His Pro His Ser Lys Ala Pro  
 275 280 285  
 Gln Ile Pro Arg Glu Asp Gly Pro Ser Pro Lys Leu Ala Leu Trp Leu  
 290 295 300  
 Pro Ser Pro Ala Pro Thr Ala Ala Pro Thr Ala Leu Gly Glu Ala Gly  
 305 310 315 320  
 Leu Ala Glu His Ser Gln Arg Asp Asp Arg Trp Leu Leu Val Ala Leu  
 325 330 335  
 Leu Val Pro Thr Cys Val Phe Leu Val Val Leu Leu Ala Leu Gly Ile  
 340 345 350  
 Val Tyr Cys Thr Arg Cys Gly Pro His Ala Pro Asn Lys Arg Ile Thr  
 355 360 365  
 Asp Cys Tyr Arg Trp Val Ile His Ala Gly Ser Lys Ser Pro Thr Glu  
 370 375 380  
 Pro Met Pro Pro Arg Gly Ser Leu Thr Gly Val Gln Thr Cys Arg Thr  
 385 390 395 400  
 Ser Val

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2473 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAGTATTGT GTCTACTTTT ATCTGTGCAC CAGCCACAAA TACCCACATT GGAAAGACCC	60
ATTTGTGATG GGTAAACATC CCTTCCTGTC TCCCACAACC CCTGTGACTG CCCTGCATGT	120
GTCATGACC TCCGAAGGCC CAAATTCTATG AAGCAGCAAA CCCAGCAGAT CTCCACCCCC	180
CTGCCTCAGG ACCTCTGCTG AAGAGGGGGA TGAAGTGGGT CTCCAGGGAG GCAGTGGGG	240
CCTTGTGCG AGCTGGCTCG GGAGCCGGCT TACAGGAGGG CAGCTCTGCA GTTGGGAGGG	300
GCACCGTCCG GAGGAGACCA GGCCTCTACA CACCCCCCAC TCTACTTATC ATCCCTGCTC	360
ACACACCCCTT GTCCAAGGCT TTATGCATCG GATTTATTTT TCCAAATCAA GAGGACAGTG	420
ATAGATGCAT TTTCCCCAGG CTGCTCAGA AAGGTCGCTA AATGTATACT GTTGTCAAGAA	480
TTGCTGAGAT CTCCCCCAC TTTGGTTTT TGCAGCAGTA AAAACTCTTT CCACTGTGAC	540
TTATTTCTC TCTCAGGCAG CCAGCCACCT GGTCCTTGT GCTGACTCTA GCACAGTGGC	600
CAGGATCCAA TACGAGTCCA GGGGTGACCG CAGGATGGTG GGGGCAGCGG GCTTCTCCAC	660
CTACCCCCAGC CACCAAGGCC CTGACGCACT GCCTCCTGCA CCTTCAGCAC ATCCCTGTGC	720
ACAGCTGGAA GGGTGCATGG CCCGCTCACC TTTGTTCAGA TGGGTGGAAA CGCTGATGAT	780
ACCAAGCTCCT CCCTGCCGTG CCCCTGCCAC GGAGCAGGCA TTGTGAACGT GCTGGTGT	840
GCAGTCCCAC GTGGCATGGC CTCCAGCCCA ACCCACAGTG GAGACTGGAG ACAGGGCAAT	900
GAGTCTGGTC GGGGCACGT GGACATGCC CATAGGGGC CCACCCAGAC TAAACAGGCA	960
AGGTCTGGGG CATTGCGCGA CGCAGGACTC AATGCTAAAG CAAGCCTGCC TGGCTCTGTG	1020
CCAGGGCCCC TCTTCTGATT TACACATCCC ATTTTACAC AGACCCTTCC TTCTTAATAA	1080
AGGCTGACAG TTCTGTTGGC AGCCAAGAAC CCACACCAG AAGACAGGGA GTGAGGGGCC	1140
TTTGTGCCCA ACTCCAGCAC AGCTGCGTTC TGGGGTGTGT GAGAGGCATG TTCGTGTCTG	1200
TGGCCTGGTG GTCTCGTGAG ACAGTTCCGA GGACGGGAA ATTGCAGGGT GGTGGGGCG	1260
TGAGGCTTAT ATGTGGAACT GATGCAGAGT TCGCCTGCAG ACGGATCTGG ATATACACTA	1320
TGTATAATTG TTACGTGTAA TTTAAAATAT ATCTGTTGTC CATCGTCATG AGAAGATTAT	1380
ATGTAAGGCT CTGAAGGGAG AGGGAGATGT ACATTCTGCC AGGCTCCTGG GGACCTTATC	1440
CGAGTCATGA AATTGATGAC TGTTGATCCA GTGGTGCAAG AAGCTACACT CCATGTGTCA	1500
TCACGCTTAT GACTCCTAAT GTATTTTAA GGCAAAAAAT GTCAGCCGAC TCCATCTTCA	1560
CCCCTCGATT CCTCGAGTCC AGCCTTTCTG TGCCAGTGCT TCACTGAGCC ACAACGCTCT	1620

CGCCATCGGG ACCCGGCTGG GCCTGGAGTC TCGGGGCACA GTTGCATGG AGCCCTCCTG	1680
GGTCATTCTA CAAATGTGCT GAGTGCCAGC TGAAAACCCC ACAGGAGATG GAGTACCTTG	1740
GCCAAGCTTA AAGAGAAGAT TTTCTCAGGG TATTTATTAG TGTGTCCAGC AGGGTCAGGA	1800
AGCAGGATGG AAAGATGCAT TCAGACTGTT AATTTATTAA CAAGGCAAAT GATTGGTGT	1860
TTCTTGATGA CAGACTATTA AGTTTGGGAC TTATTTCCC ATTTGAGAAG TTATAATATA	1920
TATTTAAGAT GATAAGTTTC CTGCTTAAGT TGTGCCTTTC AGCTTCAATG AGTTTAAGGA	1980
GCACTAAGGG TAATGATACC AATGAGGGTT GGTTTATTAT CAAACCTGAA TAGCTGTGGT	2040
TTCTCCAGTA AATATTTCT TCTACTGAAC ATGGAGCCAT TATTAAGAGT TGTGTGTTT	2100
TTATTATGTA CATTGTATA TTTTTTGCT TGTGTGATGT TCTATTTTC TAATAGTTT	2160
CTTTTAGTTT CTTAAAGTTG TGATACTAGA TTTAGATTCT GATGCTAACT GCAAATCAGG	2220
TTGGTCTCTG CTGGGTCTCT CCTGCTTTA TTTTACTTTA AGGACAAGTG TAGTTGTCGT	2280
CCACCACTT TCAAAAAATG TGAAACTGCC CTGCCTCCCC TTTTGCTGA CAACACTGTG	2340
TACATTGACC ACTTCCTACC ATACTTTATG TTGTAAAATC AAACTCTTT GTGGTACATT	2400
ATCTCATGCT TCTGCAAATT CGAATAAAATT CTATGGCTTC CAAAAAAA AAAAAAAA	2460
AAAAAAAAAA AAA	2473

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Ile Asp Ala Phe Ser Pro Gly Cys Leu Arg Lys Val Ala Lys Cys			
1	5	10	15
Ile Leu Leu Ser Glu Leu Leu Arg Ser Pro Pro Thr Phe Gly Phe Cys			
20	25	30	
Ser Ser Lys Asn Ser Phe His Cys Asp Leu Phe Ser Leu Ser Gly Ser			
35	40	45	
Gln Pro Pro Gly Pro Leu Cys			

50

55

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4093 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTAATTTTT TGTATTTTA GTAGAGATGG GGTTTCACCA CACTGGCCAG GCTTGTCTCG	60
CTCGAACCTTC TGACCTCATG ATCCACCTGC CTCGGCCTCC CAAAGTGCTG GGATTACAGG	120
TGTGAGCCAC CGCACCTGGC AAAAGAGAAT CTTACAGAAC CTATTCACTG GGAAGGAAGC	180
CCTCATTATA ATGATTTCA TTCTTATGTG TGTTTCAGGA CGACTGGGTT TGGATTCAAGA	240
AGAGGATTAT TATAACCAC AAAAGGTGGA TGTTCCAAG GCCTTGATTA TTGTTGCAGT	300
TCAATGTGGC TGTGATGGGA CATTTCTGTT GACCCAGTCA GGCAAAGTGC TGGCCTGTGG	360
ACTCAATGAA TTCAATAAGC TGGGTCTGAA TCAGTGCATG TCGGGAAATTA TCAACCATGA	420
AGCATACCAT GAAGTTCCCT ACACAACGTC CTTTACCTTG GCCAAACAGT TGTCCCTTTA	480
TAAGATCCGT ACCATTGCC CAGGCAAGAC TCACACAGCT GCTATTGATG AGCGAGGCCG	540
GCTGCTGACC TTTGGCTGCA ACAAGTGTGG GCAGCTGGC GTTGGGAACt ACAAGAAGCG	600
TCTGGGAATC AACCTGTTGG GGGGACCCCT TGGTGGGAAG CAACTGATCA GGGTCTCCTG	660
CGGTGATGAG TTTACCATTG CTGCCACTGA TGATAATCAC ATTTTGCTT GGGCAATGG	720
TGGTAATGGC CGCCTGGCAA TGACCCCCAC AGAGAGACCA CATGGCTCTG ATATCTGTAC	780
CTCATGGCCT CGGCCTATTT TTGGATCTCT GCATCATGTC CCGGACCTGT CTTGCCGTGG	840
ATGGCATAACC ATTCTCATCG TTGAGAAAGT ATTGAATTCT AAGACCATCC GTTCCAATAG	900
CAGTGGCTTA TCCATTGGAA CTGTGTTCA GAGCTCTAGC CCGGGAGGAG GCGCGGGGG	960
CGGCGGTGGT GAAGAAGAGG ACAGTCAGCA GGAATCTGAA ACTCCTGACC CAAGTGGAGG	1020
CTTCCGAGGA ACAATGGAAG CAGACCGAGG AATGGAAGGT TTAATCAGTC CCACAGAGGC	1080
CATGGGAAAC AGTAATGGGG CCAGCAGCTC CTGTCCTGGC TGGCTTCGAA AGGAGCTGGA	1140

AAATGCAGAA TTTATCCCCA TGCCTGACAG CCCATCTCCT CTCAGTGCAG CGTTTCAGA	1200
ATCTGAGAAA GATACCCTGC CCTATGAAGA GCTGCAAGGA CTCAAAGTGG CCTCTGAAGC	1260
TCCTTGGAA CACAAACCCC AAGTAGAACG CTCGTCACCT CGGCTGAATC CTGCAGTAAC	1320
CTGTGCTGGG AAGGAAACAC CACTGACTCC TCCTGCGTGT GCGTGCAGCT CTCTGCAGGT	1380
GGAGGTTGAG AGATTGCAGG GTCTGGTGT AAAGTGTCTG GCTGAACAAC AGAAGCTACA	1440
GCAAGAAAAC CTCCAGATTT TTACCCAATC GCAGAACATTG ACAAGAAAT TAGAAGGAGG	1500
GCAGCAGGTG GGGATGCATT CCAAAGGAAC TCAGACAGCA AAGGAAGAGA TGGAAATGGA	1560
TCCAAAGCCT GACTTCGATT CAGATTCCCTG GTGCCTCCTG GGAACAAACT CCTGTAGACC	1620
CAGCCTCTAT TCTCCTGAGC CTATAGAGCC CCCAGGAGAC TGGGACCCAA AGAACTTCAC	1680
AGCACACTTA CCGAATGCAG AGAGCAGCTT TCCTGGCTTT GTTCACTTGC AGAAAAGGAG	1740
CGCAAGGCAG AGGCTCTGAA GCACCTTCCT TGTACATTTG GAGAGTGGCA TTGCCTTTA	1800
GATAGGATCT AGGAGTGATT TTATGTGTTT GGAGAATGGA AGGGCCCCA TGGCCCTGGC	1860
TTTGTCATCA GTGACTGCCA TAGAACACAGC AGCTCTGTAC CTCATCTGTT GATCCCACCT	1920
TTGAAGAGGA GACACAGTGC TCACCTTAAT TGCGCTGGTA GCAGCTTATA TCCCATGTAT	1980
CATTTTCACC ATTGATTGGA AGCTGCCTTG GGAATTCACT ACCAGGCATT ACCCCTCTGG	2040
GTGGGAGAGG GAGAAGTGTA AAGTTGGAGT GGGCTGGAAT CAGGTGTGGC CCGCCCAGTG	2100
TCCTCTGCAG AGTGGTGAAG TAGCTCTGGCC CTCTTGGGAG CCCTGAGTCC AGAAAATAT	2160
GTCTGATGGA GTCAATCTAG GGCTGTGTTG GAAAAAGTTC AGTTACTCTG TGCAGCTAAA	2220
TGCTTTAGGA GGAAAGGTAG GCTTAGGTTG CTTTCCCTCT GAGGGTTGAT TGAAATTCT	2280
TCAGTGAGGA ATAGAGAAAG GGCAGGACCC TCATCATCAC ACAGCTGGTG TTTCAGGCTG	2340
TGACCAATGC AGGGTGGGAT TTCCTAACTG TGGATGAGGG GATGAGGTGT CTCTGAGGGA	2400
TGAGGTGTCT CAGAGAATTG AGTCATGGG GCAGTCAGAA TAGCCTTAAG AGAAAATCAT	2460
GAAGGAGAAG AGGTCCCTCCT TTAGCTGCCT CTACTTGGTA TCTTAGAGAG GGCTTAGAGG	2520
GCTCTCAGTC TTCTGCCCAT GAAAAGACTT CTTTGAGCCT CTGCCTCAT GGCTCTTAGG	2580
GTTCCTGATCT TGATATCAGC AGCCCCAACC ACTTTCTTC TGAATGTCTA GTCACTTATTT	2640
TTCCCCTTTT GGTGTTTAT GAAGCCATGT GGTAACGAAT GAATCTGTAT CATTTTCCT	2700
ACCTGAGTGG CCCAAAGCCA GCACCAAACC CTGGGAGTCC CTGAAGCCTA ACAGAACAGG	2760
TAGAACTTGC AAAAGGAATT TGGCTGAGAG CTCACTTCTA ATCCTGTACT CACTGTGTCT	2820

TTGTAGATAG AAACAAGCTA GCTTTACCAA AGAGAAATAG TGTCATAGAA GAACAAA	ACT 2880
TCATATAGAA AGTTCTAGGC AAGTATTGTA TGTTTCCTT AAGGATGTGA GCTTTGTATT 2940	
TCCACCTAGC CTTGTAAAAT GTTCCTGTGG TATTTTGTTG CACACATCCT ACCTTTGATG 3000	
AGTCTCACAT CCCACCTTCC TATAAACAGC TAAATTAATT TTGTTTCATC TTCCCCAGAC 3060	
CAAAATGTTT GATAATCTTA TCAACATTGT GGGAGGTCTT GTGCAATGGA AATTTGCCA 3120	
TTTCTCCAAA ACTGGTGGCA TAAAGGCTGA TGCTTGGGGA GAACCCCATT GCTCGGGACA 3180	
GGCAACTCTG TTCAATGGGA TCTTCCTTGG TTTGATGTT CCATTGTTT CTCAGTTCTG 3240	
GGAAGCCTAG TACATTAGTA CTAATGTAAT CACTGAAACC TTTTCTTGAA ATAAGGAAAG 3300	
CAGCCAAACT TTGATTAAG TTGCAAGTTC TGCGGACTTG CGGGGGTTGT CATAAACTGT 3360	
AACAGTGGGT TTTGGTTCAAG CATGTAATG CAACTTGAT TTTCTTGAGG ACCGATTGAC 3420	
CTGTCATGTC CCTGTATCCT CATGCTCATC ATCTCAGCAG GCCTGAGAGG CTGGGTCAGT 3480	
TTGGGTGTT TCATGAGGA TTGCTTCTGC CATGGAGCTG ATGGACGTGG GCAGGTTGCT 3540	
GAGAAGGTGG GGTGAAAGTG AGTGCAGGGG GTGGGTGAGT GCCCTGGTCT TGTTCATAGG 3600	
GGAGCCTTTC CCTAGCAGTG GAACGCTGTG GTCATTTCT CTAGCATATT CCCTTGGAA 3660	
GTCTAGATTT GCTATTAATC TGGCTGAGAA TCTAAGTTCT GTGCCTTAGA GACAGTTGC 3720	
ACTTTCCCCT ATTGTGCCTG GGACAGCCAT ATGATTTTT TTCCCACCAA ACAAGTATGC 3780	
AAACAGAAAC CAGTTTCAAA GGGGGATGGA GTAAAAGATG AGGCAGTAGA AATGCCCTTG 3840	
AATGGTTTTT CTGTAGCTAA TTCTCTTAA ATTTTGTCCCT GCTTTTTTC TTTATGCAGT 3900	
GCTAGGTGTT TTAAGTTTC TAGTAGTATT GCTTTTGAGT TACAGTATAA CCTGAGTTAC 3960	
TCCTCTGCTC TAACATTGTT GCAGAAGAGT AACTCAGGTT ATTGTTAGCC AGGTTGCTTG 4020	
AAAGGTTGAG AGTGGAGTGG TTTGGCATTG CTGTTTAAA TAAACATTAA AGCTCTTAAA 4080	
AAAAAAAAAAA AAA 4093	

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 522 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ile Phe Ile Leu Met Cys Val Ser Gly Arg Leu Gly Leu Asp Ser  
 1                       5                       10                       15  
  
 Glu Glu Asp Tyr Tyr Thr Pro Gln Lys Val Asp Val Pro Lys Ala Leu  
 20                      25                       30  
  
 Ile Ile Val Ala Val Gln Cys Gly Cys Asp Gly Thr Phe Leu Leu Thr  
 35                      40                       45  
  
 Gln Ser Gly Lys Val Leu Ala Cys Gly Leu Asn Glu Phe Asn Lys Leu  
 50                      55                       60  
  
 Gly Leu Asn Gln Cys Met Ser Gly Ile Ile Asn His Glu Ala Tyr His  
 65                      70                       75                       80  
  
 Glu Val Pro Tyr Thr Thr Ser Phe Thr Leu Ala Lys Gln Leu Ser Phe  
 85                      90                       95  
  
 Tyr Lys Ile Arg Thr Ile Ala Pro Gly Lys Thr His Thr Ala Ala Ile  
 100                     105                       110  
  
 Asp Glu Arg Gly Arg Leu Leu Thr Phe Gly Cys Asn Lys Cys Gly Gln  
 115                     120                       125  
  
 Leu Gly Val Gly Asn Tyr Lys Lys Arg Leu Gly Ile Asn Leu Leu Gly  
 130                     135                       140  
  
 Gly Pro Leu Gly Gly Lys Gln Val Ile Arg Val Ser Cys Gly Asp Glu  
 145                     150                       155                       160  
  
 Phe Thr Ile Ala Ala Thr Asp Asp Asn His Ile Phe Ala Trp Gly Asn  
 165                     170                       175  
  
 Gly Gly Asn Gly Arg Leu Ala Met Thr Pro Thr Glu Arg Pro His Gly  
 180                     185                       190  
  
 Ser Asp Ile Cys Thr Ser Trp Pro Arg Pro Ile Phe Gly Ser Leu His  
 195                     200                       205  
  
 His Val Pro Asp Leu Ser Cys Arg Gly Trp His Thr Ile Leu Ile Val  
 210                     215                       220  
  
 Glu Lys Val Leu Asn Ser Lys Thr Ile Arg Ser Asn Ser Ser Gly Leu  
 225                     230                       235                       240  
  
 Ser Ile Gly Thr Val Phe Gln Ser Ser Ser Pro Gly Gly Gly Gly  
 245                     250                       255  
  
 Gly Gly Gly Gly Glu Glu Asp Ser Gln Gln Glu Ser Glu Thr Pro  
 260                     265                       270  
  
 Asp Pro Ser Gly Gly Phe Arg Gly Thr Met Glu Ala Asp Arg Gly Met

275	280	285
Glu Gly Leu Ile Ser Pro Thr Glu Ala Met Gly Asn Ser Asn Gly Ala		
290	295	300
Ser Ser Ser Cys Pro Gly Trp Leu Arg Lys Glu Leu Glu Asn Ala Glu		
305	310	315
Phe Ile Pro Met Pro Asp Ser Pro Ser Pro Leu Ser Ala Ala Phe Ser		
325	330	335
Glu Ser Glu Lys Asp Thr Leu Pro Tyr Glu Glu Leu Gln Gly Leu Lys		
340	345	350
Val Ala Ser Glu Ala Pro Leu Glu His Lys Pro Gln Val Glu Ala Ser		
355	360	365
Ser Pro Arg Leu Asn Pro Ala Val Thr Cys Ala Gly Lys Gly Thr Pro		
370	375	380
Leu Thr Pro Pro Ala Cys Ala Cys Ser Ser Leu Gln Val Glu Val Glu		
385	390	395
Arg Leu Gln Gly Leu Val Leu Lys Cys Leu Ala Glu Gln Gln Lys Leu		
405	410	415
Gln Gln Glu Asn Leu Gln Ile Phe Thr Gln Leu Gln Lys Leu Asn Lys		
420	425	430
Lys Leu Glu Gly Gly Gln Gln Val Gly Met His Ser Lys Gly Thr Gln		
435	440	445
Thr Ala Lys Glu Glu Met Glu Met Asp Pro Lys Pro Asp Phe Asp Ser		
450	455	460
Asp Ser Trp Cys Leu Leu Gly Thr Asn Ser Cys Arg Pro Ser Leu Tyr		
465	470	475
Ser Pro Glu Pro Ile Glu Pro Pro Gly Asp Trp Asp Pro Lys Asn Phe		
485	490	495
Thr Ala His Leu Pro Asn Ala Glu Ser Ser Phe Pro Gly Phe Val His		
500	505	510
Leu Gln Lys Arg Ser Ala Arg Gln Arg Leu		
515	520	

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1601 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCGACGAGG CCTTCGACCA TGAGGTCTCC GCCTTCTTCC CCGCCAACCT GGACTTCCTG	60
TGCCTGCAGG AGGTGTTGA CAAGCGAGCA GCCACCAAAT TGAAAGAGCA GCTGCACGGC	120
TACTTCGAGT ACATCCTGTA CGACGTCGGG GTCTACGGCT GCCAGGGCTG CTGCAGCTTC	180
AAGTGTCTCA ACAGCGGCCT CCTCTTGCC AGCCGCTACC CCATCATGGA CGTGGCCTAT	240
CACTGTTACC CCAACAAAGTG TWACKACSAT GCCCTGGCCT CTAAGGGAGC TCTGTTCTC	300
AAGGTGCAGG TGGGAAGCAC ACCTCAGGAM CAAARAATCG TCGGGTACAT CGCCTGCACA	360
CACCTGCATG CCCCGCAAGA GGACAGCGCC ATCCGGTGTG GGCAGCTGGA CCTGCTTCAG	420
GACTGGCTGG CTGATTTCCG AAAATCTACC TCCTCGTCCA GCGCAGCCAA CCCCAGGGAG	480
CTGGTGGCAT TTGACGTCGT CTGTGGAGAT TTCAACTTTG ATAAC TGCTC CTCTGACGAC	540
AAGCTGGAGC AGCAACACTC CCTGTTCACCC CACTACAGGG ACCCCTGCCG CCTGGGGCCT	600
GGTGAGGAGA AGCCGTGGC CATCGGTACT CTGCTGGACA CGAACGGCCT GTACGATGAG	660
GATGTGTGCA CCCCCGACAA CCTGCAGAAG GTCCTGGAGA GTGAGGAGGG CCGCAGGGAG	720
TACCTGGCGT TTCCCACCAAG CAAGAGCTCG GGCCAGAAGG GGCGGAAGGA GCTGCTGAAG	780
GGCAACGGCC GGCGCATCGA CTACATGCTG CATGCAGAGG AGGGGCTGTG CCCAGACTGG	840
AAGGCCGAGG TGGAAGAATT CAGTTTATC ACCCAGCTGT CCGGCCTGAC GGACCACYTG	900
CCAGTAGCCA TGCGACTGAT GGTGTCTTCG GGGGAGGAGG AGGCATAGAC CGTCGGAGC	960
AGCGGGGCYT CTGCCAGCCC TTGCAGCTGC AGCCCATCCC TGGGCCATGT CCCCTCCATC	1020
GAGTGCCCGG TGCTTGGGGG AGGAGGGCAG GGACAGGGAG GGAGCCACAG TCAGTGCCCG	1080
GGAACCTGGA AGCTGCGCTG CTCTGCGCCT CTGGGCCTCA CTGTGGSCAG AGGAGTCAGG	1140
CCCGCCCCAG GAGCCTCCAG CTGCCCTAACCC AGTGCCTATT CTTCACAAACA CGATTTCTA	1200
CAAATCTACA GCACAACCGA GTTTGTAACC CGTGGGTTAG TATGAGGACC GGGTTCGTGT	1260
ACTCTCTGTA TCTCCTCTTA AGCTTCGTCC AGGGTTCTTT ATTTTTGTCT GCTGCCAATG	1320
TCGTCTCGCA TGCCTGCACC CTCGCATGCA CGCTGCCCGC ATGCCACGTG CCACGCTGTA	1380
GCCACAGACC CCTTGCTCGG GCCTCACCCCA AGGCCAAACT CCAAACACAA TCAGAACAG	1440

CCAAAGAACG ACTTCCTGGG CACGCCACC AGCTCTCCCG CCTCCAGTGT GGGCCGGCTC	1500
CTGCAGGGTC CGAGGGCTGC ATCTCTACCA GCCAGCCCAG GGCTCTTCCC AGGGTCTCGC	1560
ATTCAAGGGC AATTACATTT TAAAAAAAAA AAAAAAAAAA A	1601

## (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Val Ala Tyr His Cys Tyr Pro Asn Lys Cys Xaa Xaa Xaa Ala			
1	5	10	15
Leu Ala Ser Lys Gly Ala Leu Phe Leu Lys Val Gln Val Gly Ser Thr			
20	25	30	
Pro Gln Xaa Gln Xaa Ile Val Gly Tyr Ile Ala Cys Thr His Leu His			
35	40	45	
Ala Pro Gln Glu Asp Ser Ala Ile Arg Cys Gly Gln Leu Asp Leu Leu			
50	55	60	
Gln Asp Trp Leu Ala Asp Phe Arg Lys Ser Thr Ser Ser Ser Ala			
65	70	75	80
Ala Asn Pro Glu Glu Leu Val Ala Phe Asp Val Val Cys Gly Asp Phe			
85	90	95	
Asn Phe Asp Asn Cys Ser Ser Asp Asp Lys Leu Glu Gln Gln His Ser			
100	105	110	
Leu Phe Thr His Tyr Arg Asp Pro Cys Arg Leu Gly Pro Gly Glu Glu			
115	120	125	
Lys Pro Trp Ala Ile Gly Thr Leu Leu Asp Thr Asn Gly Leu Tyr Asp			
130	135	140	
Glu Asp Val Cys Thr Pro Asp Asn Leu Gln Lys Val Leu Glu Ser Glu			
145	150	155	160
Glu Gly Arg Arg Glu Tyr Leu Ala Phe Pro Thr Ser Lys Ser Ser Gly			
165	170	175	
Gln Lys Gly Arg Lys Glu Leu Leu Lys Gly Asn Gly Arg Arg Ile Asp			

180

185

190

Tyr	Met	Leu	His	Ala	Glu	Glu	Gly	Leu	Cys	Pro	Asp	Trp	Lys	Ala	Glu
					195			200				205			
Val	Glu	Glu	Phe	Ser	Phe	Ile	Thr	Gln	Leu	Ser	Gly	Leu	Thr	Asp	His
	210					215				220					
Leu	Pro	Val	Ala	Met	Arg	Leu	Met	Val	Ser	Ser	Gly	Glu	Glu	Glu	Ala
	225					230			235			240			

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCGTTGCTG	GTGCGAGTCC	TTAGGAACCA	GAATAGCATT	TCTCAGTGGG	TTCCAGTATG	60
CAGCCGATTG	ATACCTGTGT	CTCCTACCCA	AGGACAGGGG	GACAGGGCTC	TGTCTCGCAC	120
TTCCCAGTGG	CCCCAGATGA	GCCAGTCCCA	AGCATGTGGT	GGATCAGAAC	AGATTCCCTGG	180
AATAGACATA	CAGCTGAATA	GGAAAGTATCA	CACCACACGT	AAGCTTTCTA	CTACCAAAGA	240
TTCCCCACAG	CCTGTTGAGG	AGAAGGTTGG	TGCTTCACA	AAGATAATAS	AAGCCATGGG	300
ATTCACGGGA	CCTTGAAAT	ACAGTAATG	GAAGATTAAG	ATTGCGGCC	TGCGCATGTW	360
TACTAGCTGT	GTGGAGAAAA	CTGACTTCGA	GGAATTCTTT	CTAAGGTGTC	AGATGCCTGA	420
TACATTCAT	TCATGGTTTC	TTATAACCT	ACTCCACGTC	TGGATGTGTC	TAGTCCGAAT	480
GAAGCAGGAA	GGCCGGAGTG	GGAAGTACAT	GTGTCGTATC	ATAGTTCATT	TTATGTGGGA	540
GGATGTTCA	CAGCGCGCA	GAGTCATGGG	GGTTAACCCC	TATATCCTGA	AGAAGAACAT	600
GATCCTCATG	ACAAATCATT	TCTATGCAGC	GATCTTGGGA	TATGATGAGG	GGATCCTTTC	660
AGATGATCAT	GGGCTGGCCG	CTGCCCTCTG	GAGAACCTTC	TTCAACCGGA	AATGTGAAGA	720
CCCTCGACAT	CTTGAATTGC	TGGTAGAGTA	TGTGAGGAAA	CAGATACAGT	ACCTGGACTC	780
CATGAACGGG	GAGGATCTGC	TTCTGACAGG	GGAGGTGAGC	TGGCGCCCTC	TAGTGGAGAA	840

GAATCCTCAG AGCATCCTGA AGCCCCATTG TCCGACTTAC AACGACGAGG GACTTTGATG	900
GGCTGGGCC CTCGGCACGGC CCGCCAGCTG GCTTCGAGGA ACCTCCAGGA GAGAAGTGCC	960
TGTTGGTCCA GGACCCCTGCA GAAAGTGGCC TGAACGTGACC TCTGAACAGC ATCTGTCAA	1020
TACCTGGCCC CATTGGTGTGTT GAGTTTCCTC TTAGTGTGCC CAGGAGTCTG ATCTGCTGGG	1080
GTACAGGGCT GGGAGAACCC CTAGCTCTCC CGGGGTGTCC TCTCCCTTAG GGGAGGCC	1140
GAGTGAGAGT CCCCCAGCAC ACACCCCCA ACCCCCTCCA GCAACTACAT GTGACTGATA	1200
GCTTTTCCCA AAGGCCAAGG AAGGGATGGT GTAGGTTCAA AAGGGAAACC CCCCAGGGCC	1260
TGCTGTGGCC TAGGAGCAGA TTGTAATGCT GCCGAGTCCG GTCGGTGACC ACGCGTTGTC	1320
CCTCGGCTTT CAGCCATGGG GTTGAGTTGG CCATTAAAAG AAACAGAGAC TTCTCTCTGC	1380
CATGGCCCTT CTTTATTCCA GGGACTTACA AACTTGCTG AGATGGTGGA CGCAGTAATG	1440
AGGGCACCGC GCAGCTCAGT TAGAGACGGA GAAAGGAAAG AGGCTGGGAT GGTCTCTGCT	1500
GCTCTTGCTT CTAGTTCATG GAGATGTGTC TCTGTTCAGG CCAAGATACA GCCAGCCAGG	1560
CCTGTCGTCT GGGACCCAGG AGGCCTCTGA TGACCAAGGG CTTTCACATC CTAAGTCATT	1620
TGGAAGGAGG CCTTGAGAAC AAAGTCACCT TTGTCACTCC CAGTGAAC TG AATGAGGAAC	1680
ATGCTGTCTC CTGCTTGCG CTCCCCTTTC ATGAGATACT GGGGAGAAGA GAACATTCC	1740
CCTGGCTTAG TTGTAGCAGA CCCAGACCTG TGCCCAGCTT TGGTCCCCCT TCCCAACTTC	1800
TGAAGCACGT GCTGCAGAGC CACCTTGGTC TGAGCACCTG AGGACCAGCC CCTCCCTCC	1860
CAGTGCGGGT CATCTCTTGGG GGGATTTCT TAAAGTGAAG AAAGGGGTG GGGAAACATA	1920
TTGCCCTCCTC CTCCCCCATC AAACCTCCTT CATTAACTT GCTATAAAAT GAGTCATATA	1980
AAGAAACTCT ATATGGGTGA GGTATATCCC ACTTCTGTGA AAACATTACA AATCAAACCG	2040
CTTCTCTCAG TTTATTTAAG ATGCTTTGT TGCGAGCGGA GCTCTAGAGT GAAGCCTCCT	2100
GTGTGTGTGT GAGATAATAA CACCTTGTAA CTCATTACAG CTGGGCACTA TTTACATAAA	2160
CCAGAGCTGA GCCAGGCAGG AATTGCTGA TTAATTATT TTTAATGGAG TGAAGTATAC	2220
CATGCACCAA AATAAACTTT ACTGTGTGTA CCTAAAAAAA AAAAAAAA AAAA	2274

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 253 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ser Gln Ser Gln Ala Cys Gly Gly Ser Glu Gln Ile Pro Gly Ile  
1 5 10 15

Asp Ile Gln Leu Asn Arg Lys Tyr His Thr Thr Arg Lys Leu Ser Thr  
20 25 30

Thr Lys Asp Ser Pro Gln Pro Val Glu Glu Lys Val Gly Ala Phe Thr  
35 40 45

Lys Ile Ile Xaa Ala Met Gly Phe Thr Gly Pro Leu Lys Tyr Ser Lys  
50 55 60

Trp Lys Ile Lys Ile Ala Ala Leu Arg Met Xaa Thr Ser Cys Val Glu  
65 70 75 80

Lys Thr Asp Phe Glu Glu Phe Leu Arg Cys Gln Met Pro Asp Thr  
85 90 95

Phe Asn Ser Trp Phe Leu Ile Thr Leu Leu His Val Trp Met Cys Leu  
100 105 110

Val Arg Met Lys Gln Glu Gly Arg Ser Gly Lys Tyr Met Cys Arg Ile  
115 120 125

Ile Val His Phe Met Trp Glu Asp Val Gln Gln Arg Gly Arg Val Met  
130 135 140

Gly Val Asn Pro Tyr Ile Leu Lys Lys Asn Met Ile Leu Met Thr Asn  
145 150 155 160

His Phe Tyr Ala Ala Ile Leu Gly Tyr Asp Glu Gly Ile Leu Ser Asp  
165 170 175

Asp His Gly Leu Ala Ala Leu Trp Arg Thr Phe Phe Asn Arg Lys  
180 185 190

Cys Glu Asp Pro Arg His Leu Glu Leu Leu Val Glu Tyr Val Arg Lys  
195 200 205

Gln Ile Gln Tyr Leu Asp Ser Met Asn Gly Glu Asp Leu Leu Leu Thr  
210 215 220

Gly Glu Val Ser Trp Arg Pro Leu Val Glu Lys Asn Pro Gln Ser Ile  
225 230 235 240

Leu Lys Pro His Ser Pro Thr Tyr Asn Asp Glu Gly Leu  
245 250

## (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TATCCATTAC GTCGACTAAT ACGTACATAA GAATTCAATC GGGCCTTGGG GCTGGCCCTG	60
AAACCTGCGA GGGGCTTCCG TCCACGTCCC CAGTGGACCT ACCACCCCTC CATCTGGAA	120
AGCAGGCCAC AGCAGCCGGA CAAAGGAAGC TCCTCAGCCT CTAGTCGCCT CTCTGTGCAT	180
GCACATCGGT CACTGATCTC GCCTACTGGC ACAGACGTGT TTATCGGCCA ACCTGACCCT	240
CACAAAAGC TACCACCGAA GTGGACAGGC CCCTACACTG TGATACTCAG CACACCAACT	300
GCAGTGAGAG TCCGAGGACT CCCCAACTGG ATCCATCGCA CCAGGGTCAA GCTCACCCCC	360
AAGGCAGCTT CTTCCCTCCAA AACATTAACA GCTAAGTGTGTT TGTCTGGCC AATTTCTCCT	420
ACCAAGTTTA ATTAACCAA CATTTCCTTC TTAAAACCAA AACACAAGGA AGACTAACCA	480
CGTGCTTCCA GGAATGGCCT GTATCTACCC AACCACTTTC TATACCTCTC TTCCAACCAA	540
AAGTCTTAAT ATGGGAATAT CCCTCACCAC GATCCTAATA CTGTCAGTAG CTGTCCTGCT	600
GTCCACAGCA GCCCCTCCGA GCTGCCGTGA GTGTTATCAG TCTTTGCACT ACAGAGGGGA	660
GATGCAACAA TACTTACTT ACCATACTCA TATAGAAAGA TCCTGTTATG GAAACTTAAT	720
CGAGGAATGT GTTGAATCAG GAAAGAGTTA TTATAAAGTA AAGAATCTAG GAGTATGTGG	780
CAGTCGTAAT GGGGCTATTT GCCCCAGAGG GAAGCAGTGG CTTTGCTTCA CCAAAATTGG	840
ACAATGGGGA GTAAACACTC AGGTGCTTGA GGACATAAAG AGAGAACAGA TTATAGCCAA	900
AGCCAAAGCC TCAAAACCAA CAACTCCCCC TGAAAATCGC CCGCGGCATT TCCATTCTT	960
TATACAAAAA CTATAAGCAG ATGCATCCCT TCCTAAGCCA GGAAAAAATC TGTTTGTAGA	1020
TCTAGGAGAA CCATTGTGCT TACCATGAAT GTGTCCAATT GTTGGGTATG CGGGGGAGCT	1080
TTATGAGTGA ACAGTGGCTG TGGGACGGGA TAGACATTCC CCCTTACTTA CAGGCATCCC	1140
AAAACCCAG ACTCACTTTC ACTCCTCAGG AATGCCCGCA GTCCTGGACA CTTACCAACT	1200

CAGTATGAGG GACGGTGTGC ATATCCCGCA AGTGGACTGA TAAAACCCAT CGGCCGTAG	1260
GTGAAAACCC GTCACCAAAC CCTAACAGTC AATGCCTCCA TAGCTGAGTG GTGCCAAGG	1320
TTACCCCTG GAGCCTGGTC TCCTTCTAAC TTAAGCTACC TCAATTGTGT CTTGTAAAA	1380
AAGGCCTGGT ACTGTACAAA CACCACTAAC CCTTATGCCG CATAACCTCCG CCTAAGTGTA	1440
CTATGCGACA ATCCTAGGAA CACCAGCTGA CAATGGACTG CCACTGACGG ATTCTGTGG	1500
ATATGGGAA CCCAGGCTTA CTCACAGCTA CCTTATCACT GGCAAGGTAC TTGCTTCCTA	1560
GGCACAAATTC AACCTGGATT CTTTTACTT CCGAAGCACC CGGGCAACAC CCTCAGAGTC	1620
CCTGTGTATG ATAACCAGAG AAAAATGATC CTTGGAGGTA GGAGGGAGCC AAAGATTGTG	1680
AGAGGACGAG TGGCCTCCGC AACGGATCAT TGAATACTAT GGTCCTGCCA CTTGGGCAGA	1740
GGATGGTTCA TGGGTTATC GCACTCCCAT ATATATGCCA AATAGAGCGA TTAGACTACA	1800
AGCTGTTCTA GAGATAATCA CTAACCAAAC TGCTCAGCC CTAGAAATGC TCGCGAACAA	1860
ACAAAACCAA ATGCGCGCG CAATTTATCA AAACAGGCTG GCCCTAGACT ACTTATTAGC	1920
AGAAGAGGGT GCGGGCTGTG GTAAGTTAA CATCTCAAAT TGCTGTCCTA ACATAGGCAA	1980
TAATGGAGAA GAGGTTCTGG AAATCGCTTC AAACATCAGA AAAGTAGCCC GTGTACCAAGT	2040
CCAAACCTGG GAGGGATGGG ACCCAGCAAA CTTCTAGGAG GGTGGTTCTC TAATTTAGGA	2100
GGATTTAAAA TGCTGGTGGG GACAGTCATT TTCATCACTG GGGTCCTCCT GTTTCTCCCC	2160
TGTGGTATCC CATTAAAATC CTTGTTGAAA CTACAGTTAA CCTCCTGACA ATCCAGATGA	2220
TGCTCCTGCT ACAGCGGCAC GATGGATACC AACCCGTCTC TCAAGAATAC CCCAAAAATT	2280
AAGTTTTCT TTTTCCAAGG TGCCCACGCC ACCCYTATGT CACGCCTGAA GTAGTTATTG	2340
AGAAAAGTCGT CCCTTTCCCC TTTTCTATAA CCAAATAGAC AGGAATGGAA GATTCCTCCTC	2400
GGGGCCTGAA AGCTTGCAGGG ATGAATAACT CCTCCTCCTC AGGCCAGTC CCAAGGTACA	2460
AACTTGCACC AGCAGCAAGA TAGCAGAGGC AGGAAGAGAG CTGGCTGGAA GACACGTACC	2520
CCCTGAAGAT CAAGAGGGAG GTGCCCTGG TACTACATAG CAGTCACGTT AGGCTGGGAC	2580
AATTCCCTGTT TACAGAGGAC TATAAAACCC CTGCCCATC CTCACTGGG GCTGATGCCA	2640
TTTTAGGCCT CAGCCTGTCT GCATGCAGGC GCTCATTAAA ACAGCATGTT GCTCCAAAAA	2700
AAAAAAAAAA A	2711

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Ala	Cys	Ile	Tyr	Pro	Thr	Thr	Phe	Tyr	Thr	Ser	Leu	Pro	Thr	Lys
1				5										10	15
Ser Leu Asn Met Gly Ile Ser Leu Thr Thr Ile Leu Ile Leu Ser Val															
				20				25						30	
Ala Val Leu Leu Ser Thr Ala Ala Pro Pro Ser Cys Arg Glu Cys Tyr															
				35			40							45	
Gln Ser Leu His Tyr Arg Gly Glu Met Gln Gln Tyr Phe Thr Tyr His															
				50		55			60						
Thr His Ile Glu Arg Ser Cys Tyr Gly Asn Leu Ile Glu Glu Cys Val															
				65		70		75						80	
Glu Ser Gly Lys Ser Tyr Tyr Lys Val Lys Asn Leu Gly Val Cys Gly															
				85		90			95						
Ser Arg Asn Gly Ala Ile Cys Pro Arg Gly Lys Gln Trp Leu Cys Phe															
				100		105				110					
Thr Lys Ile Gly Gln Trp Gly Val Asn Thr Gln Val Leu Glu Asp Ile															
				115		120			125						
Lys Arg Glu Gln Ile Ile Ala Lys Ala Lys Ala Ser Lys Pro Thr Thr															
				130		135			140						
Pro Pro Glu Asn Arg Pro Arg His Phe His Ser Phe Ile Gln Lys Leu															
				145		150		155			160				

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2892 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGATTATTGA	GCATAACTGA	TGAGAGAATG	ACAGTATTGG	TGACTAGCTT	TTTTGTTTTT	60
AAATAACACA	CTTTAAAATG	CCACAGTGTT	ATTTGAAAGC	TTAAAGGCAT	TTTCTCATCT	120
TCAGTATTG	CTTTTTATCA	GTTGTAGAAA	AGAACCTTAG	TGTTTCTTC	TCTACCTATG	180
TATGCTTATG	AAACCGCTCT	ACCTACATAT	GAAACTTCTC	TACCTATGTA	TGTTTACGAA	240
AAGAGATGTA	TTTGCCAAGA	AAATCTTGAT	TATATAAAAG	ACAAAAAGAT	TATAAAAGAC	300
AGTTTCTGTT	TAAGTAAAAC	TGTCTTGAA	ACTTAAGAAA	GCTTAAGTTT	AAAAAAATC	360
TCAGTTAAC	ATCATTGGTT	TATTTGACTT	ACTGTTAACT	CTTGCTTCTC	TTGACTCCA	420
TGGTGTTTTT	AGATAACCAT	GTATGAACCTT	TATGTTAATG	GTTTGTGGGA	TACTAAAATA	480
GCTTGAAGAT	GACTTGATGA	CTGTGCATTT	TATATAGTTT	TATTCTCCTA	AAATCTCAGG	540
AGGGCAGCAA	GTGCTGTCAA	CGATTATATA	GTGATGAGAT	TTTTATGGGA	ATGATTCTT	600
CTTGGTGCCT	TTTACACATT	TGTACTGATA	GCAAAACTAA	AGTTAAAGC	AGCAAAGTTT	660
AAGTTCTCCT	AAATCCTAC	AGAAACCAAC	CTTTTAAGGA	CATAATTCA	TCTAAAACAT	720
GACGATATT	AGCACACCTT	TTAATGTGGG	TATATATCAA	GTGTTAAGG	ACTGGCTAGT	780
ATGTGATAGA	GCAAGACCTG	AGACTTTATA	AGTATTGCT	CGTGTCTGTT	GACAGACCTC	840
TTTCTTCAA	ACTTGTTAGA	AGAGTGGTAA	GACATATCCA	ATTGGAAAAT	AAGATGCAGT	900
GTTGTATAGC	ACATACATT	AAAGTGCTTG	CGTTAAAATT	AGTTCTCAA	TAAGATAAAA	960
TTATTTTAAA	AATTTGGTTC	ACTTTATTAC	AATAGTGGCA	ATTTAGCTTT	TCAGTATTAC	1020
AGGAATTAA	AAATTGGTTT	CTTGTAGGGG	ACATCTCAAC	TTTGGGAATA	TCTTCACTTA	1080
ATTTTTAAA	AATATTTCA	TGCTTTATTG	TCCAGCTATA	CAATATATCG	CAAATCCTG	1140
ACAAGTTCAT	TGTATTAAGG	TATTAACTAT	TACATGGAAA	GCAATTCTGT	TCATCTTTG	1200
ATGTTTGTGT	TGAAAATGCT	TATCTTGTTG	TTTGATCTT	CCAACAGCTG	AGAGCTTGAA	1260
CTGATTTAAA	CATTTGTCAA	TATACTTAAG	AATGCTTTAA	GTAAAGAAGG	GGAAAATTTT	1320
AAGTAAGTTT	TTTCCCTTCT	AGGAAGAAAA	ACTATGATGA	TGTTAAGAAA	ATGTCATTAT	1380
AGAGCTTGCT	CAATAATATG	TTCTTTAAAT	CCACCTCCAT	TTGTACATTA	TAGGTATCAT	1440
TCTGTTTTTG	CTTAAAATAA	TCTGCAACCA	TTTCAGATAG	TTTACAGCA	AATTGATCTA	1500
AAAGCCACTA	ATAAATTCTA	GGGTTTGAGT	CTAGAAGCCA	AGCAAACGT	CACCAATGTC	1560
AGTTGTAAAT	TAGAATGCAA	CATGAGGCTT	CAGACTCATG	ACAATGATAT	ACATGAAAAC	1620

AAAAATATAA TTGTGTCTAC CTTCCCTACTT TCCCTTTGA CATATGAGT TGGAATTAA	1680
CATAGCTTA AAATCCATAT TTAGAACCTT ACCTGTTCT ATAATAATTA GTAAAATGCC	1740
AAAGTAGTGA TAGAATATTG TGGCATTGAA GTAGCCGAAA AATTGTTAGT TTTAGCATCA	1800
AAAAAGTAAA TAGATGTTGA AATGAATTAA TGTATGTGCC AGGTTGAAGA GAGTGTGCCA	1860
GTGACAGGAA GTAGTCTAAA AAATTAACAG TTATGGTTT AATAGGATCT GAAAGACAAT	1920
CTTTAAAGAA ATGGGAGAAA TTGGGGTAT CAGTGAACCT ATACCAACCT CTCTTGAC	1980
ATAAAATATGG TGATGTAGCT AGATATAAAA ATCAGTGTCT TACTGGCACC ATTTACAGTT	2040
TAGAAAACAA TCTTTTCTT AAAAATGCC ATCTGATTTC TATTTTTAGG AGCTACTTGG	2100
ATTTGTATGT ATTTTTCTA CGTGAAAATA TATGTAACCT TCACCTTTGT TCCAGTACTA	2160
TAATTGCTCA TGCACCTTT CTCCCCTTG AGAACATTCA GTGAAATACA ACTTCATCAA	2220
AGATTTGCTC AAAGGAGAAG AATCGCATGA GTGTGAAAG TAGATGCTCG TAGCCAGAAC	2280
AGAAAAGGTT ACACATGATC ATGGCACAGA AGATAGGAGG TTTGACTTGG TGGCCATAA	2340
TGTTTATTAT CCTTTTGAA ATAACAGGGA CCAGCAGCAG TTTCTCAGG ATAAATGCTC	2400
TACCCCACCTT CTCTATGAAC AGGTGTGGGG AGGCTTACTT TCCATTTCATA TATTTATACA	2460
CCTCTCTACA AAAGCAATTAA TTAATGAAGG TTAGTGGAAAT TGTTAAAAT CTGAGAGGAA	2520
TGATGACTGG AGGTGTTGG GGTTTTTTTC TGTATTCAATT TTTTAATGAG AAAAGTTTA	2580
AATGTAGTAC AGGTTAGACC CAACTACTAC CTTACTATTA TAGGACGATT CTATGTTCT	2640
GTTAAAGTAT TCAAGTAGCT TTCTCTGGGG GAAAAAGTAC CACTTGACCA CTTAAAGGAA	2700
TTGGGATTTT TGTCTACTTT GGATAAGGCA GTTGACTTCT TAAGTAAAG CAATAGTGTAA	2760
AAATGTCATT TTGTTTGAA TGTAAAGTGA GCAAATAAAA AACATGTTGA AATTGTAAAA	2820
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2880
AAAAAAAAAA AA	2892

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 100 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Ile	Met	Ala	Gln	Lys	Ile	Gly	Gly	Leu	Thr	Trp	Trp	Ala	Ile	Met
1						5				10				15	
Phe	Ile	Ile	Leu	Phe	Glu	Ile	Thr	Gly	Thr	Ser	Ser	Ser	Phe	Leu	Arg
						20			25					30	
Ile	Asn	Ala	Leu	Pro	His	Phe	Ser	Met	Asn	Arg	Cys	Glu	Ala	Tyr	
						35		40				45			
Phe	Pro	Phe	Ser	Tyr	Leu	Tyr	Thr	Ser	Leu	Gln	Lys	Gln	Phe	Leu	Met
						50		55			60				
Lys	Val	Ser	Gly	Ile	Val	Lys	Asn	Leu	Arg	Gly	Met	Met	Thr	Gly	Gly
						65		70		75			80		
Val	Trp	Gly	Phe	Phe	Leu	Tyr	Ser	Phe	Phe	Asn	Glu	Lys	Ser	Phe	Lys
						85			90			95			
Cys	Ser	Thr	Gly												
			100												

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 618 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATTCGTTACA AACATGTTTG CATGCCTACC ATATCTCAGG CACTGGGGAT ACAGCAGATC	60
AAGATCCTAC CCCATGGAAC TAAAAGAGGA CAGAGTACTG AGTGGAACAT ACGATGATAG	120
ATTTACAAAT AATGTAGCAT ACTTCTACTT CATTGTATCT TAAGTTCTT GAAATATTGC	180
TACTGGAGAT TGGAAAGAAA TCTTAATGTT ATGGGGTATT GTCTAAGAAG CTTTATTTA	240
AAACCACATCTC ATTAAATTTT GTTGCATTTT AGATAATCGT CCCCAGATGC CATGTTACCC	300
TAGTGCAGAG TTTGGGGCTG GATAAGTTTT TGTTGTAGGT GGCTATCCTG TGTTTTGTAG	360
GGTATTCTAGC AGCATCCTGG CCTTAAACAA AAAATGTTTT CAGACATTGC CAAATGTCCC	420
CCGAGCGGTA AAGTCACCCCC CAAGTTGAGA ACCGCTCTAT ACAAAAGAGCT GTTATTAGAG	480

CTAGACATTT CTGAATTGGC ATCAATTCT ATATTGTATC CATAAACATT AGTAGCCACG	540
AAAAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	600
AAAAAAAAAA AAAAAAAA	618

## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Phe Ser Asp Ile Ala Lys Cys Pro Pro Ser Gly Lys Val Thr Pro	
1 5 10 15	
Lys Leu Arg Thr Ala Leu Tyr Lys Glu Leu Leu Leu Glu Leu Asp Ile	
20 25 30	
Ser Glu Leu Ala Ser Ile Ser Ile Leu Tyr Pro	
35 40	

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 772 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TGCCATACAC TTCAGCAGAG TTTGCAACTT CTCTTCTAAG TCTTTATCCT TCCCCCAAGG	60
CATGCCTAGG ACAGGACTCT TGAAACAGTGA TGCCTCAATT AGAGTTGCTA GCCAATAGAT	120
TGAAGCTATG TTGGCACAAAT ATCCTACATC CTCCCGATCT ACTGGCTGAG CCCAACCCCA	180
CCTAAGAAGG ACAATAAAGA TCTGTGTTCA GAGTCATACT GAATAGAGAC TTCTGGACTC	240
TATAGAACCC ACTGCCTCCT GATGAAGTCC CTACTGTTCA CCCTTGAGT TTTTATGCTC	300

CTGGCCCAAT TGGTCTCAGG TAATTGGTAT GTGAAAAAGT GTCTAACGA CGTTGGAATT	360
TGCAAGAAGA AGTGCAAACC TGAAGAGATG CATGTAAAGA ATGGTIGGGC AATGTGCGGC	420
AAACAAAGGG ACTGCTGTGT TCCAGCTGAC AGACGTGCTA ATTATCCTGT TTTCTGTGTC	480
CAGACAAAGA CTACAAGAAT TTCAACAGTA ACAGCAACAA CAGCAACAAAC AACTTTGATG	540
ATGACTACTG C'TTCGATGTC TTCGATGGCT CCTACCCGTT TCTCCCACTG GTTGAACATT	600
CCAGCCTCTG TCTCCTGCTC TAGGATCCCC GACTCATTAAGCAGAAAGAGG CTTAAAAAAA	660
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	720
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA	772

## (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 131 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln	
1 5 10 15	
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly	
20 25 30	
Ile Cys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly	
35 40 45	
Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg	
50 55 60	
Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile	
65 70 75 80	
Ser Thr Val Thr Ala Thr Ala Thr Thr Thr Leu Met Met Thr Thr	
85 90 95	
Ala Ser Met Ser Ser Met Ala Pro Thr Arg Phe Ser His Trp Leu Asn	
100 105 110	
Ile Pro Ala Ser Val Ser Cys Ser Arg Ile Pro Asp Ser Leu Lys Gln	
115 120 125	

Arg Gly Leu  
130

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 875 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCTGTTTCA ATATTTATA ATGAAAATT TTGAACATTC GGAGAACGGT AAAGAATTAC	60
ACCCAGAACCA CCCATGTCTA CCATGTTACT ACATTTGTGT GTGTGTGTGT GTGTGTGTGT	120
GTGTGCGTGT GCAATTTAA TTACAATGGT CGAGGAAGCT CTTGCTGAGA AGGTGATGTT	180
GAATAAAGAC TCTAAAGACC CTAAGAGTT GAGAGAGAGC TGTGTGGAGT TCTGGGCC	240
AGGCACAGCA AGTACAAAGA TCCTGAAGCA GGAGCATTCT TGGTGTGTTC AAGGAAAGCA	300
AGGAGGCCAG TGAGGTTGGA AAAGGAAATG AGGTCAGART AATAATAGGG TGAAAGARGA	360
TGGCTGGGGG ATGGGGGGC ARTGARGCAG GGCCTATGGT TTCTACTTGG TGARGTGGGA	420
ARCCACTGGA RGGGTTAAC CCGATAATTG ATGTCACATA ATTTATGTTG TAATGGAACC	480
CGTGTGACTG CTCCTGGGA ACAGACAAAA GAAAGGGTAG TAGAGACACC AGCTAGGAAG	540
CAGATTCAAGC TAGAAGAGAT GATACCTTCC ACTAAGGTGT TGGAGAACGT GTTGGATTCT	600
AGATAATTTT TGAAGGTGGA GTTGGCAGAA TTTGAAGATC ATTCCATTTC TGTTCATACA	660
GAGCTTCCTC ATTCTCTTT GACAGCTGCC TAGAATCTCA TTGTATCATA ATGTTTAAA	720
CTAGTCCCCG ATGATGAATA TTTAGGTTGA TGCTTCTCT CTTGCTGCCA CAAAACAGAC	780
ATATATTTGT ATAAAATGCC ACGTGGACAT GTCATTCTTC ACATAAGTGA GTATTTGTAG	840
AATAAATTCC AAGAACAGA AAAAAAAA AAAAA	875

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 79 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Ser Thr Met Leu Leu His Leu Cys Val Cys Val Cys Val Cys Val  
1 5 10 15

Cys Ala Cys Ala Ile Leu Ile Thr Met Val Glu Glu Ala Leu Ala Glu  
20 25 30

Lys Val Met Leu Asn Lys Asp Ser Lys Asp Pro Lys Glu Leu Arg Glu  
35 40 45

Ser Cys Val Glu Phe Trp Gly Pro Gly Thr Ala Ser Thr Lys Ile Leu  
50 55 60

Lys Gln Glu His Ser Trp Cys Val Gln Gly Lys Gln Gly Gly Gln  
65 70 75

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TNCACGATGCC CAGTGCAAGC AGGACCAC

29

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TNGGACAAGGG TGTGTGAGCA GGGATGAT

29

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GNGCTTCCTTC CCAGTGAATA GGTTCTGT

29

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ANAAACTCGGT TGTGCTGTAG ATTTGTAG

29

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ANGAACTAGAG GCAAGAGCAG CAGAGACC

29

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ANCTCTTCCT GATTCAACAC ATTCCCTCG

29

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CNCTCATGCGA TTCTTCTCCT TTGAGCAA

29

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ANCTCTGCACT AGGGTAACAT GGCATCTG

29

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GNGTGAACAGT AGGGACTTCA TCAGGAGG

29

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ANTGTAGTAAC ATGGTAGACA TGGGTGTT

29

What is claimed is:

1. An isolated polynucleotide selected from the group consisting of:
  - (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
  - (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 65 to nucleotide 1270;
  - (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 1139 to nucleotide 1270;
  - (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 1011 to nucleotide 1216;
  - (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BO114\_1 deposited under accession number ATCC 98333;
  - (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BO114\_1 deposited under accession number ATCC 98333;
  - (g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone BO114\_1 deposited under accession number ATCC 98333;
  - (h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone BO114\_1 deposited under accession number ATCC 98333;
  - (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
  - (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 196 to amino acid 205 of SEQ ID NO:2;
  - (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
  - (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and
  - (m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.
3. A host cell transformed with the polynucleotide of claim 2.
4. The host cell of claim 3, wherein said cell is a mammalian cell.
5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:
  - (a) growing a culture of the host cell of claim 3 in a suitable culture medium; and
  - (b) purifying said protein from the culture.
6. A protein produced according to the process of claim 5.
7. The protein of claim 6 comprising a mature protein.
8. A protein comprising an amino acid sequence selected from the group consisting of:
  - (a) the amino acid sequence of SEQ ID NO:2;
  - (b) the amino acid sequence of SEQ ID NO:2 from amino acid 326 to amino acid 384;
  - (c) fragments of the amino acid sequence of SEQ ID NO:2 comprising the amino acid sequence from amino acid 196 to amino acid 205 of SEQ ID NO:2; and
  - (d) the amino acid sequence encoded by the cDNA insert of clone BO114\_1 deposited under accession number ATCC 98333;the protein being substantially free from other mammalian proteins.
9. The protein of claim 8, wherein said protein comprises the amino acid sequence of SEQ ID NO:2.
10. The protein of claim 8, wherein said protein comprises the amino acid sequence of SEQ ID NO:2 from amino acid 326 to amino acid 384.

11. A composition comprising the protein of claim 8 and a pharmaceutically acceptable carrier.

12. A method for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition of claim 11.

13. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:1.

14. An isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 418 to nucleotide 582;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 508 to nucleotide 582;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 1 to nucleotide 555;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CD311\_2 deposited under accession number ATCC 98333;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CD311\_2 deposited under accession number ATCC 98333;

(g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone CD311\_2 deposited under accession number ATCC 98333;

(h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone CD311\_2 deposited under accession number ATCC 98333;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:4;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:4;

- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and
- (m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

15. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:4;
- (b) the amino acid sequence of SEQ ID NO:4 from amino acid 1 to amino acid 46;
- (c) fragments of the amino acid sequence of SEQ ID NO:4 comprising the amino acid sequence from amino acid 22 to amino acid 31 of SEQ ID NO:4; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CD311\_2 deposited under accession number ATCC 98333;

the protein being substantially free from other mammalian proteins.

16. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:3.

17. An isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 191 to nucleotide 1756;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 254 to nucleotide 1756;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 1 to nucleotide 604;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CG279\_1 deposited under accession number ATCC 98333;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CG279\_1 deposited under accession number ATCC 98333;

- (g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone CG279\_1 deposited under accession number ATCC 98333;
- (h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone CG279\_1 deposited under accession number ATCC 98333;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 256 to amino acid 265 of SEQ ID NO:6;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and
- (m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

18. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:6;
- (b) the amino acid sequence of SEQ ID NO:6 from amino acid 1 to amino acid 138;
- (c) fragments of the amino acid sequence of SEQ ID NO:6 comprising the amino acid sequence from amino acid 256 to amino acid 265 of SEQ ID NO:6; and
- (d) the amino acid sequence encoded by the cDNA insert of clone CG279\_1 deposited under accession number ATCC 98333;

the protein being substantially free from other mammalian proteins.

19. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:5.

20. An isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 226 to nucleotide 948;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 1128 to nucleotide 1601;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CJ424\_9 deposited under accession number ATCC 98333;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CJ424\_9 deposited under accession number ATCC 98333;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone CJ424\_9 deposited under accession number ATCC 98333;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone CJ424\_9 deposited under accession number ATCC 98333;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:8;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

21. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;

(b) fragments of the amino acid sequence of SEQ ID NO:8 comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:8; and

(c) the amino acid sequence encoded by the cDNA insert of clone CJ424\_9 deposited under accession number ATCC 98333; the protein being substantially free from other mammalian proteins.

22. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:7.

23. An isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 137 to nucleotide 895;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 1488 to nucleotide 2274;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CR930\_1 deposited under accession number ATCC 98333;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CR930\_1 deposited under accession number ATCC 98333;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone CR930\_1 deposited under accession number ATCC 98333;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone CR930\_1 deposited under accession number ATCC 98333;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 121 to amino acid 130 of SEQ ID NO:10;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

24. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:10;
- (b) fragments of the amino acid sequence of SEQ ID NO:10 comprising the amino acid sequence from amino acid 121 to amino acid 130 of SEQ ID NO:10; and
- (c) the amino acid sequence encoded by the cDNA insert of clone CR930\_1 deposited under accession number ATCC 98333;

the protein being substantially free from other mammalian proteins.

25. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:9.

26. An isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 494 to nucleotide 973;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 611 to nucleotide 973;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 521 to nucleotide 940;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone DA306\_4 deposited under accession number ATCC 98333;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone DA306\_4 deposited under accession number ATCC 98333;
- (g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone DA306\_4 deposited under accession number ATCC 98333;

- (h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone DA306\_4 deposited under accession number ATCC 98333;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 75 to amino acid 84 of SEQ ID NO:12;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and
- (m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

27. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:12;
- (b) the amino acid sequence of SEQ ID NO:12 from amino acid 11 to amino acid 149;
- (c) fragments of the amino acid sequence of SEQ ID NO:12 comprising the amino acid sequence from amino acid 75 to amino acid 84 of SEQ ID NO:12; and
- (d) the amino acid sequence encoded by the cDNA insert of clone DA306\_4 deposited under accession number ATCC 98333;

the protein being substantially free from other mammalian proteins.

28. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:11.

29. An isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 2295 to nucleotide 2594;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 1867 to nucleotide 2372;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone DG76\_1 deposited under accession number ATCC 98333;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone DG76\_1 deposited under accession number ATCC 98333;
- (f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone DG76\_1 deposited under accession number ATCC 98333;
- (g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone DG76\_1 deposited under accession number ATCC 98333;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:14;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and
- (l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

30. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
- (b) the amino acid sequence of SEQ ID NO:14 from amino acid 1 to amino acid 26;
- (c) fragments of the amino acid sequence of SEQ ID NO:14 comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:14; and

(d) the amino acid sequence encoded by the cDNA insert of clone DG76\_1 deposited under accession number ATCC 98333;  
the protein being substantially free from other mammalian proteins.

31. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:13.

32. An isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 394 to nucleotide 522;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 1 to nucleotide 476;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone DO19\_1 deposited under accession number ATCC 98333;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone DO19\_1 deposited under accession number ATCC 98333;

(f) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone DO19\_1 deposited under accession number ATCC 98333;

(g) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone DO19\_1 deposited under accession number ATCC 98333;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 16 to amino acid 25 of SEQ ID NO:16;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ; and

(l) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i).

33. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
- (b) the amino acid sequence of SEQ ID NO:16 from amino acid 1 to amino acid 27;
- (c) fragments of the amino acid sequence of SEQ ID NO:16 comprising the amino acid sequence from amino acid 16 to amino acid 25 of SEQ ID NO:16; and
- (d) the amino acid sequence encoded by the cDNA insert of clone DO19\_1 deposited under accession number ATCC 98333;

the protein being substantially free from other mammalian proteins.

34. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:15.

35. An isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 262 to nucleotide 654;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 322 to nucleotide 654;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 1 to nucleotide 618;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone EQ219\_1 deposited under accession number ATCC 98333;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone EQ219\_1 deposited under accession number ATCC 98333;
- (g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone EQ219\_1 deposited under accession number ATCC 98333;

- (h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone EQ219\_1 deposited under accession number ATCC 98333;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 60 to amino acid 69 of SEQ ID NO:18;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and
- (m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

36. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:18;
- (b) the amino acid sequence of SEQ ID NO:18 from amino acid 1 to amino acid 119;
- (c) fragments of the amino acid sequence of SEQ ID NO:18 comprising the amino acid sequence from amino acid 60 to amino acid 69 of SEQ ID NO:18; and
- (d) the amino acid sequence encoded by the cDNA insert of clone EQ219\_1 deposited under accession number ATCC 98333;

the protein being substantially free from other mammalian proteins.

37. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:17.

38. An isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 74 to nucleotide 310;

- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 125 to nucleotide 310;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 1 to nucleotide 338;
- (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone FG340\_1 deposited under accession number ATCC 98333;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone FG340\_1 deposited under accession number ATCC 98333;
- (g) a polynucleotide comprising the nucleotide sequence of the mature protein coding sequence of clone FG340\_1 deposited under accession number ATCC 98333;
- (h) a polynucleotide encoding the mature protein encoded by the cDNA insert of clone FG340\_1 deposited under accession number ATCC 98333;
- (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:20;
- (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;
- (l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ; and
- (m) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(j).

39. A protein comprising an amino acid sequence selected from the group consisting of:

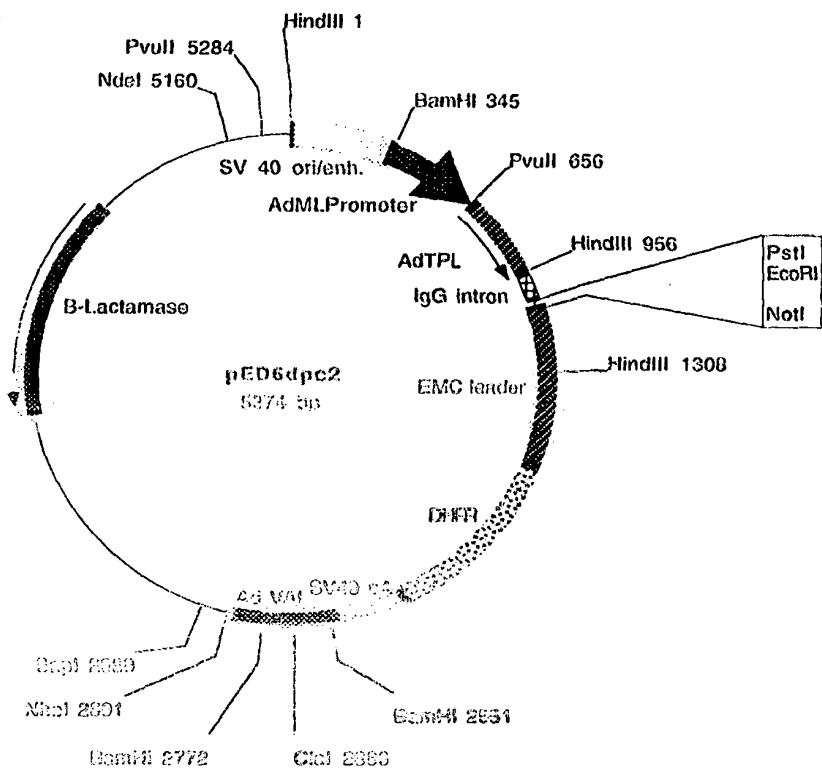
- (a) the amino acid sequence of SEQ ID NO:20;
- (b) the amino acid sequence of SEQ ID NO:20 from amino acid 1 to amino acid 75;

(c) fragments of the amino acid sequence of SEQ ID NO:20 comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:20; and

(d) the amino acid sequence encoded by the cDNA insert of clone FG340\_1 deposited under accession number ATCC 98333; the protein being substantially free from other mammalian proteins.

40. An isolated gene corresponding to the cDNA sequence of SEQ ID NO:19.

## FIGURE 1A

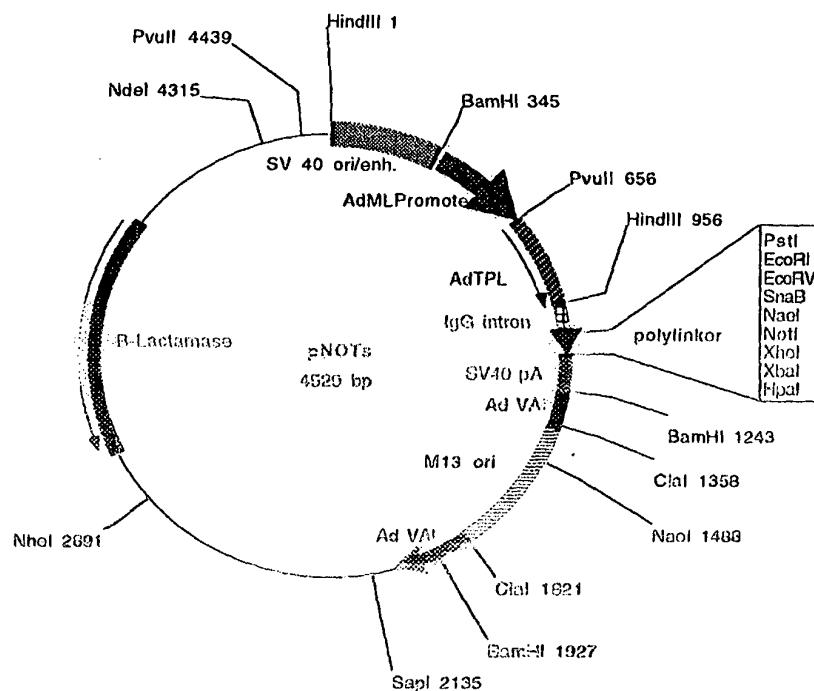


Plasmid name: pED6dpc2

Plasmid size: 5374 bp

**Comments/References:** pED6dpc2 is derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning. SST cDNAs are cloned between EcoRI and NotI. pED vectors are described in Kaufman et al.(1991), NAR 19: 4485-4490.

FIGURE 1B



**Plasmid name:** pNOTs

**Plasmid size:** 4529 bp

**Comments/References:** pNOTs is a derivative of pMT2 (Kaufman et al, 1989. Mol. Cell. Biol. 9:1741-1750).

DHFR was deleted and a new polylinker was inserted between EcoRI and HpaI. M13 origin

of replication was inserted in the ClaI site. SST cDNAs are cloned between EcoRI and

NotI